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Run on: April 12, 2006, 05:20:02 ; Search time 2287.11 Seconds
(without alignments)
986.217 Million cell updates/sec

Sequence: 1 acaactggtacatctgcgcg.....ggagcaatgagatltacacg 560

Searched: 9281099 beqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18561424

Post-processing: Listing first 1000 summaries

Database : Published Applications_NA_New:*

- 1: /SID5/ptodata/2/pubnua/US06 NEW PUB. seq.*
- 2: /SID5/ptodata/2/pubnua/US06 NEW PUB. seq.*
- 3: /SID5/ptodata/2/pubnua/US07 NEW PUB. seq.*
- 4: /SID5/ptodata/2/pubnua/PCT NEW PUB. seq.*
- 5: /SID5/ptodata/2/pubnua/US09 NEW PUB. seq.*
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- 11: /SID5/ptodata/2/pubnua/US11 NEW PUB. seq.*
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- 14: /SID5/ptodata/2/pubnua/US11 NEW PUB. seq.*
- 15: /SID5/ptodata/2/pubnua/US06 NEW PUB. seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

C	19	1	3.2	369	6	US-09-925-065A-539147	Sequence 539147,
C	20	18	3.2	359	6	US-09-925-065A-539148	Sequence 539148,
C	21	18	3.2	476	9	US-10-301-480-42504	Sequence 42504, A
C	22	18	3.2	476	9	US-10-301-480-42505	Sequence 42505, A
C	23	18	3.2	476	9	US-10-301-480-655913	Sequence 655913,
C	24	18	3.2	476	6	US-10-301-480-655914	Sequence 655914,
C	25	18	3.2	498	6	US-09-925-065A-144381	Sequence 144381,
C	26	18	3.2	507	10	US-10-301-480-238954	Sequence 238954,
C	27	18	3.2	507	10	US-10-301-480-825363	Sequence 852363,
C	28	18	3.2	509	10	US-10-301-480-310231	Sequence 310231,
C	29	18	3.2	509	10	US-10-301-480-310232	Sequence 310232,
C	30	18	3.2	509	10	US-10-301-480-923640	Sequence 923640,
C	31	18	3.2	509	10	US-10-301-480-923641	Sequence 923641,
C	32	18	3.2	512	6	US-09-925-065A-435208	Sequence 435208,
C	33	18	3.2	512	10	US-10-301-480-497941	Sequence 497941,
C	34	18	3.2	522	10	US-10-301-480-111350	Sequence 111350,
C	35	18	3.2	524	6	US-09-925-065A-225679	Sequence 225679,
C	36	18	3.2	524	6	US-09-925-065A-225680	Sequence 225680,
C	37	18	3.2	549	6	US-09-925-065A-398800	Sequence 398800,
C	38	18	3.2	562	10	US-10-301-480-466193	Sequence 466193,
C	39	18	3.2	562	10	US-10-301-480-1079602	Sequence 1079602,
C	40	18	3.2	573	10	US-10-301-480-30386	Sequence 30386,
C	41	18	3.2	573	6	US-10-301-480-9121265	Sequence 9121265,
C	42	18	3.2	579	6	US-09-925-065A-217603	Sequence 217603,
C	43	18	3.2	632	6	US-09-925-065A-725515	Sequence 725515,
C	44	18	3.2	635	6	US-09-925-065A-800539	Sequence 800539,
C	45	18	3.2	635	6	US-09-925-065A-800540	Sequence 800540,
C	46	18	3.2	652	10	US-10-301-480-295571	Sequence 295571,
C	47	18	3.2	652	10	US-10-301-480-295572	Sequence 295572,
C	48	18	3.2	652	10	US-10-301-480-295573	Sequence 295573,
C	49	18	3.2	652	10	US-10-301-480-908980	Sequence 908980,
C	50	18	3.2	652	10	US-10-301-480-908981	Sequence 908981,
C	51	18	3.2	652	10	US-10-301-480-908982	Sequence 908982,
C	52	18	3.2	658	6	US-09-925-065A-207982	Sequence 207982,
C	53	18	3.2	658	6	US-09-925-065A-207983	Sequence 207983,
C	54	18	3.2	658	6	US-09-925-065A-207984	Sequence 207984,
C	55	18	3.2	680	10	US-10-301-480-566514	Sequence 566514,
C	56	18	3.2	680	10	US-10-301-480-1179923	Sequence 1179923
C	57	18	3.2	684	6	US-09-925-065A-543177	Sequence 543177,
C	58	18	3.2	816	8	US-10-750-185-63180	Sequence 63180, A
C	59	18	3.2	816	8	US-10-750-623-53180	Sequence 63180, A
C	60	18	3.2	866	10	US-10-301-480-556845	Sequence 556845,
C	61	18	3.2	866	10	US-10-301-480-5170254	Sequence 5170254
C	62	18	3.2	914	6	US-09-925-065A-57029	Sequence 57029, A
C	63	18	3.2	914	6	US-09-925-065A-57030	Sequence 57030, A
C	64	18	3.2	914	6	US-09-925-065A-57030	Sequence 57030, A
C	65	18	3.2	914	9	US-10-301-480-158266	Sequence 158266,
C	66	18	3.2	914	9	US-10-301-480-158267	Sequence 158267,
C	67	18	3.2	914	9	US-10-301-480-158268	Sequence 158268,
C	68	18	3.2	914	10	US-10-301-480-771675	Sequence 771675,
C	69	18	3.2	914	10	US-10-301-480-771676	Sequence 771676,
C	70	18	3.2	914	10	US-10-301-480-771677	Sequence 771677,
C	71	18	3.2	1024	11	US-11-345-147-10	Sequence 10,
C	72	18	3.2	1187	9	US-10-301-480-40213	Sequence 40213, A
C	73	18	3.2	1187	9	US-10-301-480-40214	Sequence 40214, A
C	74	18	3.2	1187	9	US-10-301-480-40215	Sequence 40215, A
C	75	18	3.2	1187	10	US-10-301-480-653623	Sequence 653622,
C	76	18	3.2	1187	10	US-10-301-480-653624	Sequence 653623,
C	77	18	3.2	1187	10	US-10-301-480-653624	Sequence 653624,
C	78	18	3.2	1380	6	US-09-925-065A-63800	Sequence 63800, A
C	79	18	3.2	1380	9	US-10-301-480-771039	Sequence 771039
C	80	18	3.2	1380	10	US-10-301-480-784448	Sequence 784448
C	81	18	3.2	1458	14	US-11-058-688-95084	Sequence 9508, A
C	82	18	3.2	1474	6	US-09-925-065A-631116	Sequence 63116, A
C	83	18	3.2	1474	6	US-09-925-065A-631117	Sequence 63117, A
C	84	18	3.2	1474	6	US-09-925-065A-631118	Sequence 63118, A
C	85	18	3.2	1474	6	US-09-925-065A-631120	Sequence 63119, A
C	86	18	3.2	1474	6	US-09-925-065A-631120	Sequence 63120, A
C	87	18	3.2	1474	9	US-10-301-480-164354	Sequence 164354,
C	88	18	3.2	1474	9	US-10-301-480-164355	Sequence 164355,
C	89	18	3.2	1474	9	US-10-301-480-164356	Sequence 164356,
C	90	18	3.2	1474	9	US-10-301-480-164357	Sequence 164357,
C	91	18	3.2	1474	9	US-10-301-480-164358	Sequence 164358,

C 92	18	3.2	1474	10	US-10-301-480-777763	Sequence 777763,	C 165	17	3.0	605	6	US-09-925-065A-13466	Sequence 13466, A
C 93	18	3.2	1474	10	US-10-301-480-777764	Sequence 777764,	C 166	17	3.0	605	6	US-09-925-065A-13467	Sequence 13467, A
C 94	18	3.2	1474	10	US-10-301-480-777765	Sequence 777765,	C 167	17	3.0	605	6	US-09-925-065A-13468	Sequence 13468, A
C 95	18	3.2	1474	10	US-10-301-480-777766	Sequence 777766,	C 168	17	3.0	605	6	US-09-925-065A-13469	Sequence 13469, A
C 96	18	3.2	1474	10	US-10-301-480-777767	Sequence 777767,	C 169	17	3.0	605	9	US-10-301-480-114703	Sequence 114703,
C 97	18	3.2	2399	6	US-09-925-065A-704454	Sequence 704454,	C 170	17	3.0	605	9	US-10-301-480-114704	Sequence 114704,
C 98	18	3.2	2399	6	US-09-925-065A-704455	Sequence 704455,	C 171	17	3.0	605	9	US-10-301-480-114705	Sequence 114705,
C 99	18	3.2	2399	6	US-09-925-065A-704456	Sequence 704456,	C 172	17	3.0	605	10	US-10-301-480-602787	Sequence 602787,
C 100	18	3.2	2902	11	US-11-245-147-85	Sequence 85, App1	C 173	17	3.0	605	10	US-10-301-480-602788	Sequence 602788,
C 101	18	3.2	2902	11	US-11-245-147-85	Sequence 85, App1	C 174	17	3.0	605	10	US-10-301-480-128112	Sequence 128112,
C 102	18	3.2	3945	9	US-10-932-182A-82661	Sequence 82661, A	C 175	17	3.0	605	10	US-10-301-480-128113	Sequence 128113,
C 103	18	3.2	3945	9	US-10-932-182A-82661	Sequence 82661, A	C 176	17	3.0	605	10	US-10-301-480-128114	Sequence 128114,
C 104	18	3.2	4335	8	US-10-949-720-394	Sequence 394, App	C 177	17	3.0	608	6	US-09-925-065A-1216196	Sequence 1216196,
C 105	18	3.2	43948	11	US-11-231-243-111	Sequence 111, App	C 178	17	3.0	611	10	US-10-301-480-273686	Sequence 273686,
C 106	18	3.2	43948	8	US-10-949-720-393	Sequence 393, App	C 179	17	3.0	611	10	US-10-301-480-887095	Sequence 887095,
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C 108	18	3.2	182303	14	US-11-121-086-45	Sequence 45, App1	C 181	17	3.0	615	6	US-09-925-065A-190124	Sequence 190124,
C 109	18	3.2	1457619	14	US-11-098-686-8739	Sequence 8739, Ap	C 182	17	3.0	616	10	US-10-301-480-266390	Sequence 266390,
C 110	18	3.2	1457619	14	US-11-098-686-8739	Sequence 8739, Ap	C 183	17	3.0	617	9	US-10-301-480-879799	Sequence 879799,
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C 113	17	3.0	19	13	US-11-083-784-151967	Sequence 1456620,	C 186	17	3.0	617	10	US-10-301-480-677222	Sequence 677222,
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C 115	17	3.0	364	6	US-09-925-065A-95723	Sequence 95723, A	C 188	17	3.0	618	10	US-10-301-480-886809	Sequence 886809,
C 116	17	3.0	425	6	US-09-925-065A-890925	Sequence 890925,	C 189	17	3.0	618	10	US-10-301-480-900218	Sequence 900218,
C 117	17	3.0	445	6	US-09-925-065A-575133	Sequence 575133,	C 190	17	3.0	621	6	US-09-925-065A-922912	Sequence 922912,
C 118	17	3.0	446	6	US-09-925-065A-263425	Sequence 263425,	C 191	17	3.0	622	6	US-09-925-065A-95966	Sequence 95966,
C 119	17	3.0	450	10	US-10-301-480-341457	Sequence 341457,	C 192	17	3.0	623	10	US-10-301-480-657462	Sequence 657462,
C 120	17	3.0	450	10	US-10-301-480-954866	Sequence 954866,	C 193	17	3.0	623	10	US-10-301-480-1080871	Sequence 1080871,
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C 136	17	3.0	580	10	US-10-301-480-460342	Sequence 460342,	C 209	17	3.0	869	6	US-09-925-065A-18901	Sequence 18901, A
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245	17	3.0	2724	9	US-10-301-480-178624	Sequence 178624,	C 318	16	2.9	380	6	US-09-925-065A-664178	Sequence 664178,
246	17	3.0	2724	9	US-10-301-480-178625	Sequence 178625,	C 319	16	2.9	397	6	US-09-925-065A-845905	Sequence 845905,
247	17	3.0	2724	10	US-10-301-480-792032	Sequence 792032,	C 320	16	2.9	398	6	US-09-925-065A-855967	Sequence 855967,
248	17	3.0	2724	10	US-10-301-480-792033	Sequence 792033,	C 321	16	2.9	404	6	US-09-925-065A-855972	Sequence 855972,
249	17	3.0	2724	10	US-10-301-480-792034	Sequence 792034,	C 322	16	2.9	408	6	US-09-925-065A-855980	Sequence 855980,
250	17	3.0	2937	6	US-09-925-065A-683424	Sequence 683424,	C 323	16	2.9	408	6	US-09-925-065A-497601	Sequence 497601,
251	17	3.0	3682	6	US-09-925-065A-1949	Sequence 1949, Ap	C 324	16	2.9	408	6	US-09-925-065A-497602	Sequence 497602,
252	17	3.0	3682	6	US-09-925-065A-1950	Sequence 1950, Ap	C 325	16	2.9	412	10	US-10-301-480-489561	Sequence 489561,
253	17	3.0	3682	6	US-09-925-065A-1951	Sequence 1951, Ap	C 326	16	2.9	412	10	US-10-301-480-1102970	Sequence 1102970,
254	17	3.0	3682	6	US-09-925-065A-1952	Sequence 1952, Ap	C 327	16	2.9	425	9	US-10-301-480-3015	Sequence 3015, Ap
255	17	3.0	3682	6	US-09-925-065A-1953	Sequence 1953, Ap	C 328	16	2.9	425	10	US-10-301-480-616424	Sequence 616424,
256	17	3.0	3682	6	US-09-925-065A-1954	Sequence 1954, Ap	C 329	16	2.9	450	9	US-10-301-480-1889	Sequence 1889, Ap
257	17	3.0	3682	9	US-09-925-065A-45661	Sequence 45661, A	C 330	16	2.9	450	10	US-10-301-480-615288	Sequence 615288,
258	17	3.0	3682	9	US-10-301-480-103186	Sequence 103186,	C 331	16	2.9	454	6	US-09-925-065A-575088	Sequence 575088,
259	17	3.0	3682	9	US-10-301-480-103187	Sequence 103187,	C 332	16	2.9	465	6	US-09-925-065A-737902	Sequence 737902,
260	17	3.0	3682	9	US-10-301-480-103188	Sequence 103188,	C 333	16	2.9	467	6	US-09-925-065A-559059	Sequence 559059,
261	17	3.0	3682	9	US-10-301-480-103189	Sequence 103189,	C 334	16	2.9	467	14	US-11-136-527-7335	Sequence 7335, Ap
262	17	3.0	3682	9	US-10-301-480-103190	Sequence 103190,	C 335	16	2.9	467	14	US-11-136-527-7335	Sequence 7335, Ap
263	17	3.0	3682	9	US-10-301-480-103191	Sequence 103191,	C 336	16	2.9	468	6	US-09-925-065A-178016	Sequence 178016,
264	17	3.0	3682	9	US-10-301-480-146899	Sequence 146899,	C 337	16	2.9	472	6	US-09-925-065A-178017	Sequence 178017,
265	17	3.0	3682	10	US-10-301-480-716595	Sequence 716595,	C 338	16	2.9	476	6	US-09-925-065A-788510	Sequence 788510,
266	17	3.0	3682	10	US-10-301-480-716596	Sequence 716596,	C 339	16	2.9	478	6	US-09-925-065A-788510	Sequence 788510,
267	17	3.0	3682	10	US-10-301-480-716597	Sequence 716597,	C 340	16	2.9	473	10	US-10-301-480-469060	Sequence 469060,
268	17	3.0	3682	10	US-10-301-480-716598	Sequence 716598,	C 341	16	2.9	473	10	US-10-301-480-882469	Sequence 882469,
269	17	3.0	3682	10	US-10-301-480-716599	Sequence 716599,	C 342	16	2.9	473	10	US-10-301-480-882470	Sequence 882470,
270	17	3.0	3682	10	US-10-301-480-716600	Sequence 716600,	C 343	16	2.9	475	6	US-09-925-065A-942356	Sequence 942356,
271	17	3.0	3787	10	US-10-301-480-760308	Sequence 760308,	C 344	16	2.9	479	10	US-10-301-480-115164	Sequence 115164,
272	17	3.0	3977	8	US-10-301-480-760308	Sequence 760308,	C 345	16	2.9	479	10	US-10-301-480-1028573	Sequence 1028573,
273	17	3.0	3977	8	US-10-750-185-55057	Sequence 55057, A	C 346	16	2.9	482	6	US-09-925-065A-139580	Sequence 139580,
274	17	3.0	4209	8	US-10-750-185-55057	Sequence 55057, A	C 347	16	2.9	485	10	US-10-301-480-334649	Sequence 334649,
275	17	3.0	4209	8	US-10-750-185-55057	Sequence 55057, A	C 348	16	2.9	485	10	US-10-301-480-848058	Sequence 848058,
276	17	3.0	6257	14	US-11-011-332A-80	Sequence 80, Appl	C 349	16	2.9	497	6	US-09-925-065A-495140	Sequence 495140,
277	17	3.0	6257	14	US-11-011-332A-80	Sequence 94, Appl	C 350	16	2.9	493	6	US-09-925-065A-477307	Sequence 477307,
278	17	3.0	7887	14	US-11-128-061-815	Sequence 815, App	C 351	16	2.9	493	6	US-09-925-065A-477308	Sequence 477308,
279	17	3.0	7887	14	US-11-128-049-815	Sequence 815, App	C 352	16	2.9	496	6	US-09-925-065A-108241	Sequence 108241,
280	17	3.0	110000	14	US-11-155-492-1	Sequence 1, Appl	C 353	16	2.9	496	10	US-10-301-480-174975	Sequence 174975,
281	17	3.0	180574	14	US-11-121-086-70	Sequence 70, Appl	C 354	16	2.9	496	10	US-10-301-480-1088384	Sequence 1088384,
282	17	3.0	197241	11	US-11-114-798-47	Sequence 47, Appl	C 355	16	2.9	498	6	US-09-925-065A-1088384	Sequence 1088384,
283	16	2.9	19	12	US-11-101-244-41365	Sequence 41365, A	C 356	16	2.9	498	6	US-09-925-065A-16435	Sequence 216435,
284	16	2.9	19	12	US-11-101-244-41393	Sequence 41393, A	C 357	16	2.9	498	6	US-09-925-065A-176117	Sequence 176117,
285	16	2.9	19	12	US-11-101-244-41396	Sequence 41396, A	C 358	16	2.9	498	10	US-10-301-480-372008	Sequence 372008,
286	16	2.9	19	12	US-11-101-244-1456605	Sequence 1456605,	C 359	16	2.9	498	10	US-10-301-480-916302	Sequence 916302,
287	16	2.9	19	13	US-11-083-784-41365	Sequence 41365, A	C 360	16	2.9	498	10	US-10-301-480-985417	Sequence 985417,
288	16	2.9	19	13	US-11-083-784-41393	Sequence 41393, A	C 361	16	2.9	499	6	US-09-925-065A-108240	Sequence 108240,
289	16	2.9	19	13	US-11-083-784-41396	Sequence 41396, A	C 362	16	2.9	499	6	US-09-925-065A-108241	Sequence 108241,
290	16	2.9	19	13	US-11-083-784-41396	Sequence 41396, A	C 363	16	2.9	499	6	US-09-925-065A-108242	Sequence 108242,
291	16	2.9	25	9	US-10-932-182A-89126	Sequence 89126, A	C 364	16	2.9	499	6	US-09-925-065A-108243	Sequence 108243,
292	16	2.9	25	9	US-10-932-182A-89126	Sequence 89126, A	C 365	16	2.9	499	6	US-09-925-065A-836343	Sequence 836343,
293	16	2.9	25	9	US-10-932-182A-89126	Sequence 89126, A	C 366	16	2.9	499	6	US-09-925-065A-836343	Sequence 836343,
294	16	2.9	25	14	US-11-121-849-71320	Sequence 71320, A	C 367	16	2.9	500	10	US-10-301-480-467667	Sequence 467667,
295	16	2.9	25	14	US-11-121-849-71321	Sequence 71321, A	C 368	16	2.9	500	10	US-10-301-480-167667	Sequence 167667,
296	16	2.9	25	14	US-11-121-849-204224	Sequence 204224, A	C 369	16	2.9	500	10	US-10-301-480-1081075	Sequence 1081075,
297	16	2.9	50	14	US-11-175-859-88823	Sequence 88823, A	C 370	16	2.9	500	6	US-10-301-480-1081076	Sequence 1081076,
298	16	2.9	200	14	US-11-098-686-4395	Sequence 4395, Ap	C 371	16	2.9	504	6	US-09-925-065A-571757	Sequence 571757,
299	16	2.9	201	8	US-10-995-561-37746	Sequence 37746, A	C 372	16	2.9	505	6	US-09-925-065A-571757	Sequence 571757,
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302	16	2.9	201	14	US-11-124-367A-9163	Sequence 9163, Ap	C 375	16	2.9	510	6	US-09-925-065A-1080325	Sequence 1080325,
303	16	2.9	347	10	US-10-301-480-269225	Sequence 269225,	C 376	16	2.9	515	9	US-10-301-480-66210	Sequence 66210, A
304	16	2.9	347	10	US-10-301-480-269226	Sequence 269226,	C 377	16	2.9	515	9	US-10-301-480-66211	Sequence 66211, A
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309	16	2.9	348	6	US-09-925-065A-178204	Sequence 178204,	C 382	16	2.9	516	10	US-10-301-480-117291	Sequence 117291,
310	16	2.9	348	6	US-09-925-065A-178205	Sequence 178205,	C 383	16	2.9	516	10	US-10-301-480-1030700	Sequence 1030700,

384	16	2.9	517	14	US-11-128-061-1532	Sequence 1532, Ap	C 457	16	551	6	US-09-925-065A-728949	Sequence 728949,
385	16	2.9	517	14	US-11-128-061-5174	Sequence 5174, Ap	C 458	16	551	10	US-10-301-480-488241	Sequence 488241,
386	16	2.9	517	14	US-11-128-049-1532	Sequence 1532, Ap	C 459	16	551	10	US-10-301-480-488242	Sequence 488242,
387	16	2.9	517	14	US-11-128-049-5174	Sequence 5174, Ap	C 460	16	551	10	US-10-301-480-488243	Sequence 488243,
C 388	16	2.9	518	9	US-09-925-065A-24476	Sequence 24476, A	C 461	16	551	10	US-10-301-480-1101630	Sequence 1101630,
C 389	16	2.9	518	9	US-10-301-480-125713	Sequence 125713, A	C 462	16	551	10	US-10-301-480-1101651	Sequence 1101651,
C 390	16	2.9	518	10	US-10-301-480-739122	Sequence 739122, A	C 463	16	551	10	US-10-301-480-1101652	Sequence 1101652,
C 391	16	2.9	520	6	US-09-925-065A-650727	Sequence 650727, A	C 464	16	552	6	US-09-925-065A-254258	Sequence 254258,
C 392	16	2.9	522	10	US-10-301-480-292785	Sequence 292785, A	C 465	16	552	6	US-09-925-065A-991076	Sequence 991076,
C 393	16	2.9	522	10	US-10-301-480-906194	Sequence 906194, A	C 466	16	555	6	US-09-925-065A-122880	Sequence 122880,
C 394	16	2.9	523	6	US-09-925-065A-400400	Sequence 400400, A	C 467	16	555	6	US-09-925-065A-743322	Sequence 743322,
C 395	16	2.9	524	6	US-09-925-065A-400401	Sequence 400401, A	C 468	16	556	6	US-09-925-065A-424105	Sequence 424105,
C 396	16	2.9	524	6	US-09-925-065A-816820	Sequence 816820, A	C 469	16	556	6	US-09-925-065A-424106	Sequence 424106,
C 397	16	2.9	526	6	US-09-925-065A-328777	Sequence 328777, A	C 470	16	556	6	US-09-925-065A-124107	Sequence 124107,
C 398	16	2.9	526	6	US-09-925-065A-328778	Sequence 328778, A	C 471	16	556	6	US-09-925-065A-658927	Sequence 658927,
C 399	16	2.9	526	6	US-09-925-065A-328779	Sequence 328779, A	C 472	16	556	6	US-10-301-480-220496	Sequence 220496,
C 400	16	2.9	526	6	US-09-925-065A-334218	Sequence 334218, A	C 473	16	556	10	US-10-301-480-833305	Sequence 833305,
C 401	16	2.9	526	6	US-09-925-065A-400402	Sequence 400402, A	C 474	16	557	6	US-09-925-065A-781102	Sequence 781102,
C 402	16	2.9	526	6	US-09-925-065A-400403	Sequence 400403, A	C 475	16	558	9	US-10-301-480-235445	Sequence 235445, A
C 403	16	2.9	526	6	US-09-925-065A-478091	Sequence 478091, A	C 476	16	558	10	US-10-301-480-636954	Sequence 636954,
C 404	16	2.9	526	14	US-11-031-356-16	Sequence 16, Ap	C 477	16	559	6	US-09-925-065A-143500	Sequence 143500,
C 405	16	2.9	527	6	US-09-925-065A-113241	Sequence 113241, A	C 478	16	559	6	US-09-925-065A-143500	Sequence 143500,
C 406	16	2.9	527	10	US-10-301-480-402711	Sequence 402711, A	C 479	16	559	9	US-10-301-480-3363	Sequence 3663, Ap
C 407	16	2.9	527	10	US-10-301-480-402712	Sequence 402712, A	C 480	16	559	10	US-10-301-480-659576	Sequence 269576,
C 408	16	2.9	527	10	US-10-301-480-402713	Sequence 402713, A	C 481	16	559	10	US-10-301-480-659578	Sequence 27282,
C 409	16	2.9	527	10	US-10-301-480-1016120	Sequence 1016120, A	C 482	16	559	10	US-10-301-480-659578	Sequence 27283,
C 410	16	2.9	527	10	US-10-301-480-1016121	Sequence 1016121, A	C 483	16	559	10	US-10-301-480-659578	Sequence 61072,
C 411	16	2.9	527	10	US-10-301-480-1016122	Sequence 1016122, A	C 484	16	559	10	US-10-301-480-882985	Sequence 882985,
C 412	16	2.9	529	6	US-09-925-065A-391684	Sequence 391684, A	C 485	16	559	10	US-10-301-480-890691	Sequence 890691,
C 413	16	2.9	534	9	US-10-301-480-208036	Sequence 208036, A	C 486	16	559	10	US-10-301-480-890692	Sequence 890692,
C 414	16	2.9	534	10	US-10-301-480-459891	Sequence 459891, A	C 487	16	561	6	US-09-925-065A-54543	Sequence 54543, A
C 415	16	2.9	534	10	US-10-301-480-1073300	Sequence 1073300, A	C 488	16	561	6	US-10-301-480-155781	Sequence 155781, A
C 416	16	2.9	535	10	US-10-301-480-414537	Sequence 414537, A	C 489	16	561	10	US-10-301-480-769190	Sequence 769190,
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C 418	16	2.9	535	10	US-10-301-480-414538	Sequence 414538, A	C 491	16	564	6	US-09-925-065A-857749	Sequence 857749,
C 419	16	2.9	535	10	US-10-301-480-1027946	Sequence 1027946, A	C 492	16	565	6	US-09-925-065A-858893	Sequence 858893,
C 420	16	2.9	536	6	US-09-925-065A-341696	Sequence 341696, A	C 493	16	566	6	US-09-925-065A-664073	Sequence 664073,
C 421	16	2.9	536	6	US-09-925-065A-486790	Sequence 486790, A	C 494	16	566	10	US-10-301-480-831817	Sequence 831817,
C 422	16	2.9	536	10	US-10-301-480-4027764	Sequence 4027764, A	C 495	16	567	6	US-09-925-065A-857821	Sequence 857821,
C 423	16	2.9	536	10	US-10-301-480-1021173	Sequence 1021173, A	C 496	16	567	6	US-09-925-065A-360016	Sequence 360016,
C 424	16	2.9	537	6	US-09-925-065A-121661	Sequence 121661, A	C 497	16	567	6	US-09-925-065A-360017	Sequence 360017,
C 425	16	2.9	537	9	US-10-301-480-208037	Sequence 208037, A	C 498	16	567	6	US-09-925-065A-360018	Sequence 360018,
C 426	16	2.9	537	9	US-10-301-480-208038	Sequence 208038, A	C 499	16	567	6	US-10-301-480-651442	Sequence 651442,
C 427	16	2.9	537	10	US-10-301-480-208039	Sequence 208039, A	C 500	16	567	10	US-10-301-480-821448	Sequence 821448,
C 428	16	2.9	537	10	US-10-301-480-821445	Sequence 821445, A	C 501	16	567	10	US-10-301-480-821445	Sequence 821445,
C 429	16	2.9	537	10	US-10-301-480-821446	Sequence 821446, A	C 502	16	569	9	US-10-301-480-212732	Sequence 212732,
C 430	16	2.9	537	10	US-10-301-480-821447	Sequence 821447, A	C 503	16	569	10	US-10-301-480-821447	Sequence 821447,
C 431	16	2.9	537	10	US-10-301-480-821448	Sequence 821448, A	C 504	16	569	10	US-10-301-480-821448	Sequence 821448,
C 432	16	2.9	537	10	US-10-301-480-821448	Sequence 821448, A	C 505	16	569	10	US-10-301-480-821448	Sequence 821448,
C 433	16	2.9	539	6	US-09-925-065A-481182	Sequence 481182, A	C 506	16	569	10	US-10-301-480-821448	Sequence 821448,
C 434	16	2.9	540	9	US-10-301-480-212433	Sequence 212433, A	C 507	16	569	10	US-10-301-480-821448	Sequence 821448,
C 435	16	2.9	540	9	US-10-301-480-825842	Sequence 825842, A	C 508	16	569	10	US-10-301-480-1044572	Sequence 1044572,
C 436	16	2.9	542	6	US-09-925-065A-376604	Sequence 376604, A	C 509	16	569	10	US-10-301-480-1044573	Sequence 1044573,
C 437	16	2.9	542	6	US-09-925-065A-376605	Sequence 376605, A	C 510	16	569	10	US-10-301-480-1044573	Sequence 1044573,
C 438	16	2.9	542	6	US-09-925-065A-376611	Sequence 376611, A	C 511	16	570	10	US-10-301-480-1204149	Sequence 1204149,
C 439	16	2.9	542	6	US-09-925-065A-376619	Sequence 376619, A	C 512	16	573	10	US-10-301-480-245573	Sequence 245573,
C 440	16	2.9	542	6	US-09-925-065A-750882	Sequence 750882, A	C 513	16	573	10	US-10-301-480-245573	Sequence 245573,
C 441	16	2.9	542	6	US-09-925-065A-823048	Sequence 823048, A	C 514	16	574	10	US-10-301-480-245566	Sequence 245566,
C 442	16	2.9	542	6	US-09-925-065A-823048	Sequence 823048, A	C 515	16	574	10	US-10-301-480-245567	Sequence 245567,
C 443	16	2.9	545	6	US-09-925-065A-589089	Sequence 589089, A	C 516	16	574	10	US-10-301-480-245567	Sequence 245567,
C 444	16	2.9	547	6	US-09-925-065A-178594	Sequence 178594, A	C 517	16	574	10	US-10-301-480-858976	Sequence 858976,
C 445	16	2.9	547	10	US-10-301-480-219912	Sequence 219912, A	C 518	16	575	6	US-09-925-065A-594223	Sequence 594223,
C 446	16	2.9	547	10	US-10-301-480-833331	Sequence 833331, A	C 519	16	575	6	US-09-925-065A-766118	Sequence 766118,
C 447	16	2.9	548	10	US-10-301-480-288592	Sequence 288592, A	C 520	16	577	6	US-09-925-065A-425923	Sequence 425923,
C 448	16	2.9	548	10	US-10-301-480-333226	Sequence 333226, A	C 521	16	577	6	US-09-925-065A-419552	Sequence 419552,
C 449	16	2.9	548	10	US-10-301-480-902001	Sequence 902001, A	C 522	16	577	6	US-09-925-065A-619553	Sequence 619553,
C 450	16	2.9	548	10	US-10-301-480-946635	Sequence 946635, A	C 523	16	579	6	US-09-925-065A-119542	Sequence 619542,
C 451	16	2.9	549	6	US-09-925-065A-151722	Sequence 151722, A	C 524	16	579	6	US-09-925-065A-620365	Sequence 620365,
C 452	16	2.9	549	6	US-09-925-065A-151723	Sequence 151723, A	C 525	16	580	6	US-09-925-065A-184183	Sequence 184183,
C 453	16	2.9	550	6	US-09-925-065A-151726	Sequence 151726, A	C 526	16	580	6	US-09-925-065A-207013	Sequence 207013,
C 454	16	2.9	551	6	US-09-925-065A-187226	Sequence 187226, A	C 527	16	580	6	US-09-925-065A-207014	Sequence 207014,
C 455	16	2.9	551	6	US-09-925-065A-187227	Sequence 187227, A	C 528	16	580	6	US-09-925-065A-207015	Sequence 207015,
C 456	16	2.9	551	6	US-09-925-065A-728948	Sequence 728948, A	C 529	16	580	6	US-09-925-065A-207016	Sequence 207016,

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C 531	16	2.9	581	10	US-10-301-480-887952	Sequence 887952,	C 604	16	2.9	605	6	US-09-925-065A-110702	Sequence 110702,
C 532	16	2.9	582	6	US-09-925-065A-436648	Sequence 436648,	C 605	16	2.9	605	6	US-09-925-065A-764529	Sequence 764529,
C 533	16	2.9	583	6	US-09-925-065A-341698	Sequence 341698,	C 606	16	2.9	605	6	US-09-925-065A-764605	Sequence 764605,
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C 535	16	2.9	583	6	US-09-925-065A-495764	Sequence 495764,	C 608	16	2.9	607	6	US-09-925-065A-887673	Sequence 887673,
C 536	16	2.9	583	10	US-10-301-480-498310	Sequence 498310,	C 609	16	2.9	608	9	US-10-301-480-89156	Sequence 89156, A
C 537	16	2.9	583	10	US-10-301-480-111719	Sequence 111719,	C 610	16	2.9	608	9	US-10-301-480-89157	Sequence 89157, A
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C 539	16	2.9	584	10	US-10-301-480-469562	Sequence 469562,	C 612	16	2.9	608	10	US-10-301-480-32465	Sequence 32465,
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C 541	16	2.9	585	6	US-09-925-065A-434114	Sequence 434114,	C 614	16	2.9	608	10	US-10-301-480-702566	Sequence 702566,
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C 564	16	2.9	591	6	US-09-925-065A-395761	Sequence 395761,	C 637	16	2.9	618	6	US-09-925-065A-855079	Sequence 855079,
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C 575	16	2.9	595	6	US-09-925-065A-400106	Sequence 400106,	C 648	16	2.9	620	9	US-10-301-480-124867	Sequence 124867,
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C 595	16	2.9	602	6	US-09-925-065A-749615	Sequence 749615,	C 668	16	2.9	624	6	US-09-925-065A-104147	Sequence 104147,
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770	16	2.9	721	10	US-10-301-480-119371	Sequence 119371, A
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ALIGNMENTS

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; TITLE OF INVENTION: Methode of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
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Query Match 3.6%; Score 20; DB 6; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 361 GAAGAGAGAAATACAAAAGT 380
|||||
Db 350 GAAGAGAGAAATACAAAAGT 369
```

```
RESULT 3
US-09-925-065A-648675
; Sequence 648675, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648675
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-648675

Query Match 3.6%; Score 20; DB 6; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
/ Sequence 223976, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/   Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 223976
/ LENGTH: 537
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-223976
```

```
Query Match          3.4%; Score 19; DB 6; Length 537;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      216 GATTGTAATGTTTAGAA 234
DB      74 GATTGTAATGTTTAGAA 56
```

```
RESULT 5
US-09-925-065A-223977/c
/ Sequence 223977, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/   Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 223977
/ LENGTH: 537
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-223977
```

```
Query Match          3.4%; Score 19; DB 6; Length 537;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      216 GATTGTAATGTTTAGAA 234
DB      74 GATTGTAATGTTTAGAA 56
```

```
RESULT 6
US-09-925-065A-643642/c
/ Sequence 643642, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/   Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 643642
/ LENGTH: 540
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-643642
```

```
Query Match          3.4%; Score 19; DB 6; Length 540;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      360 AGAGAGAGAAATACAAA 378
DB      476 AGAGAGAGAAATACAAA 458
```

```
RESULT 7
US-10-301-480-308848/c
/ Sequence 308848, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/   in the Human Genome
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 308848
/ LENGTH: 545
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-308848
```

```
Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      216 GATTGTAATGTTTAGAA 234
DB      82 GATTGTAATGTTTAGAA 64
```

```
RESULT 8
US-10-301-480-308849/c
```

```
/ Sequence 308849, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 308849
/ LENGTH: 545
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-308849

Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      216 GATTGTAATGTTTAGAA 234
Db      82 GATTGTAATGTTTAGAA 64

RESULT 9
US-10-301-480-922257/C
/ Sequence 922257, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 922257
/ LENGTH: 545
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-922257

Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      216 GATTGTAATGTTTAGAA 234
Db      82 GATTGTAATGTTTAGAA 64

RESULT 10
US-10-301-480-922258/C
/ Sequence 922258, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ CURRENT FILING DATE: 2002-11-21
```

```
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 922258
/ LENGTH: 545
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-922258

Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      216 GATTGTAATGTTTAGAA 234
Db      82 GATTGTAATGTTTAGAA 64

RESULT 11
US-11-079-463-724
/ Sequence 724, Application US/11079463
/ Publication No. US20060073161A1
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
/ FILE REFERENCE: PATH00-03DIV2
/ CURRENT APPLICATION NUMBER: US/11/079,463
/ CURRENT FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/128,705
/ PRIOR FILING DATE: 1999-04-09
/ PRIOR APPLICATION NUMBER: US 09/540,209
/ PRIOR FILING DATE: 2000-04-04
/ NUMBER OF SEQ ID NOS: 10444
/ SEQ ID NO 724
/ LENGTH: 564
/ TYPE: DNA
/ ORGANISM: B. fragilis
US-11-079-463-724

Query Match          3.4%; Score 19; DB 11; Length 564;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 GAAGTAGCTGAAGCTTTCA 286
Db      283 GAAGTAGCTGAAGCTTTCA 301

RESULT 12
US-09-925-065A-906587/C
/ Sequence 906587, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
```



```
; SEQ ID NO 5201
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-5201
```

```
Query Match
Best Local Similarity 100.0%; Pred.No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 348 TAAAGAGTTGAGAGA 365
Db 188 TAAAGAGTTGAGAGA 171
```

```
RESULT 17
US-09-925-065A-539145/C
; Sequence 539145, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 539145
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539145
```

```
Query Match
Best Local Similarity 100.0%; Pred.No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 117 TGATTAGAGCAGAAGC 134
Db 238 TGATTAGAGCAGAAGC 221
```

```
RESULT 18
US-09-925-065A-539146/C
; Sequence 539146, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
```

```
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 539146
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539146
```

```
Query Match
Best Local Similarity 100.0%; Pred.No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 117 TGATTAGAGCAGAAGC 134
Db 238 TGATTAGAGCAGAAGC 221
```

```
RESULT 19
US-09-925-065A-539147/C
; Sequence 539147, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 539147
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539147
```

```
Query Match
Best Local Similarity 100.0%; Pred.No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 117 TGATTAGAGCAGAAGC 134
Db 238 TGATTAGAGCAGAAGC 221
```

```
RESULT 20
US-09-925-065A-539148/C
; Sequence 539148, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
```

```

; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 539148
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539148

Query Match
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TGATTAGACGAGC 134
DB 238 TGATTAGACGAGC 221

RESULT 21
US-10-301-480-42504
; Sequence 42504, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42504
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-42504

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198

RESULT 22
US-10-301-480-42505
; Sequence 42505, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42505
; LENGTH: 476
; TYPE: DNA

; ORGANISM: Homo sapien
US-10-301-480-42505

Query Match
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198

RESULT 23
US-10-301-480-655913
; Sequence 655913, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 655913
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-655913

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198

RESULT 24
US-10-301-480-655914
; Sequence 655914, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 655914
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-655914

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198
```

Db 181 AAAATGATTCAAGCAAA 198

RESULT 25

```
US-09-925-065A-144381
; Sequence 144381, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144381
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-144381
```

Query Match 3.2%; Score 18; DB 6; Length 498;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 ATCAATTATCTTCCAAA 187

Db 307 ATCAATTATCTTCCAAA 324

RESULT 26

```
US-10-301-480-238954
; Sequence 238954, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238954
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-238954
```

Query Match 3.2%; Score 18; DB 10; Length 507;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 ATCAATTATCTTCCAAA 187

Db 316 ATCAATTATCTTCCAAA 333

RESULT 27

```
US-10-301-480-852363
; Sequence 852363, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 852363
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-852363
```

Query Match 3.2%; Score 18; DB 10; Length 507;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 ATCAATTATCTTCCAAA 187

Db 316 ATCAATTATCTTCCAAA 333

RESULT 28

```
US-10-301-480-310231
; Sequence 310231, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310231
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-310231
```

Query Match 3.2%; Score 18; DB 10; Length 509;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATAATTCTAGAATTCA 408

Db 488 GATAATTCTAGAATTCA 505

RESULT 29

```
US-10-301-480-310232
; Sequence 310232, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
```

```
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310232
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-310232

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTCA 408
DB 488 GATTAATTCGAAATTCA 505

RESULT 30
US-10-301-480-923640
; Sequence 923640, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923640
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-923640

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTCA 408
DB 488 GATTAATTCGAAATTCA 505

RESULT 31
US-10-301-480-923641
; Sequence 923641, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923641
```

```
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-923641

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTCA 408
DB 488 GATTAATTCGAAATTCA 505

RESULT 32
US-09-925-065A-436208
; Sequence 436208, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436208
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-436208

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTCA 408
DB 334 GATTAATTCGAAATTCA 351

RESULT 33
US-10-301-480-497941
; Sequence 497941, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497941
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapien
```


US-10-301-480-497941

Query Match 3.2%; Score 18; DB 10; Length 522;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTTCA 408

Db 344 GATTAATTCGAAATTTCA 361

RESULT 34

US-10-301-480-1111350

Sequence 1111350, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1111350

LENGTH: 522

TYPE: DNA

ORGANISM: Homo sapiens

US-10-301-480-1111350

Query Match 3.2%; Score 18; DB 10; Length 522;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTTCA 408

Db 344 GATTAATTCGAAATTTCA 361

RESULT 35

US-09-925-065A-225679

Sequence 225679, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 225679

LENGTH: 524

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-225679

Query Match 3.2%; Score 18; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTTCA 408

Db 503 GATTAATTCGAAATTTCA 520

RESULT 36

US-09-925-065A-225680

Sequence 225680, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 225680

LENGTH: 524

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-225680

Query Match 3.2%; Score 18; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATTAATTCGAAATTTCA 408

Db 503 GATTAATTCGAAATTTCA 520

RESULT 37

US-09-925-065A-398800

Sequence 398800, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 398800

LENGTH: 549

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-398800

Query Match 3.2%: Score 18; DB 6; Length 549;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TTGGAGTGATTTGTAATG 226

DB 69 TTGGAGTGATTTGTAATG 86

RESULT 38

US-10-301-480-466193
; Sequence 466193, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466193
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-466193

Query Match 3.2%: Score 18; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TTGGAGTGATTTGTAATG 226

DB 69 TTGGAGTGATTTGTAATG 86

RESULT 39

US-10-301-480-1079602
; Sequence 1079602, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1079602
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1079602

Query Match 3.2%: Score 18; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TTGGAGTGATTTGTAATG 226

DB 69 TTGGAGTGATTTGTAATG 86

RESULT 40

US-10-301-480-303856
; Sequence 303856, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303856
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-303856

Query Match 3.2%: Score 18; DB 10; Length 573;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 TTTTAGAGATCATATG 244

DB 543 TTTTAGAGATCATATG 560

Search completed: April 12, 2006, 07:07:31
Job time : 2296.11 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 16:27:36 ; Search time 7710.45 Seconds
(without alignments)
3398.084 Million cell updates/sec

Title: US-10-712-654-34

Perfect score: 560
Sequence: 1 acaactgcgtacatctgcgcg.....ggagcaatgagaattacacg 560

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	3.8	346	9	AQ237761 RPI11-64
C 2	21	3.8	436	1	AM069787 cr50e08.x
C 3	21	3.8	557	9	CE052269 C19r-gss-
C 4	21	3.8	559	5	BM646686 BM646686
C 5	21	3.8	582	8	DR421506 DR421506
C 6	21	3.8	609	9	AQ237789 CCH37E08
C 7	21	3.8	637	10	CE361611 RPI11-64
C 8	21	3.8	779	11	CR825238 CR825238
C 9	21	3.8	902	2	DNS50945 DNS50945
C 10	20	3.6	208	2	BF475913 BF475913
C 11	20	3.6	220	10	AG191545 AG191545
C 12	20	3.6	326	8	CX630648 CX630648
C 13	20	3.6	352	8	CX630668 CX630668
C 14	20	3.6	471	2	AQ832728 HS_3238_A
C 15	20	3.6	471	2	BF843865 NM1-HT18
C 16	20	3.6	480	7	CN846247 PG07010P1
C 17	20	3.6	546	2	BE65726 BE65726
C 18	20	3.6	556	3	BM289207 BM289207
C 19	20	3.6	558	5	AQ702954 HS_5443_B
C 20	20	3.6	587	5	BM220108 BM220108
C 21	20	3.6	594	5	BM355953 BM355953
C 22	20	3.6	599	8	DT014963 DT014963

C 23	20	3.6	650	10	CL347309
C 24	20	3.6	652	8	DT014681
C 25	20	3.6	721	1	AF062715
C 26	20	3.6	721	1	A1110607
C 27	20	3.6	774	10	AG594544
C 28	20	3.6	797	9	B2717132
C 29	20	3.6	815	9	CC855478
C 30	20	3.6	974	6	CBS58744
C 31	20	3.6	1175	9	BH770411
C 32	19	3.4	140	7	CN351365
C 33	19	3.4	173	2	BI033292
C 34	19	3.4	231	3	BI315574
C 35	19	3.4	239	5	BX501946
C 36	19	3.4	354	2	BE695762
C 37	19	3.4	357	7	CO174612
C 38	19	3.4	386	2	BI123660
C 39	19	3.4	399	1	AL911633
C 40	19	3.4	399	3	BM024201
C 41	19	3.4	400	3	BI534176
C 42	19	3.4	404	1	AM466723
C 43	19	3.4	408	7	CNS71020
C 44	19	3.4	414	10	C2810619
C 45	19	3.4	425	1	AM566806
C 46	19	3.4	425	3	BI880748
C 47	19	3.4	427	1	AV412280
C 48	19	3.4	427	3	BI534292
C 49	19	3.4	437	2	BG729141
C 50	19	3.4	440	1	AA148431
C 51	19	3.4	443	5	BQ628382
C 52	19	3.4	448	7	CR792402
C 53	19	3.4	455	3	BI428905
C 54	19	3.4	457	6	CD860340
C 55	19	3.4	459	1	A1588145
C 56	19	3.4	463	3	BI706193
C 57	19	3.4	470	10	CW411105
C 58	19	3.4	482	1	AM527707
C 59	19	3.4	495	7	CR536667
C 60	19	3.4	498	7	CNS32415
C 61	19	3.4	517	10	CU915556
C 62	19	3.4	522	5	BY479743
C 63	19	3.4	527	1	AM154791
C 64	19	3.4	533	7	CR774267
C 65	19	3.4	538	2	BE941710
C 66	19	3.4	538	3	BI706265
C 67	19	3.4	539	1	AL911634
C 68	19	3.4	555	7	CN492456
C 69	19	3.4	560	9	AQ245104
C 70	19	3.4	562	7	CNS23288
C 71	19	3.4	567	6	CAB15328
C 72	19	3.4	573	7	CNS15164
C 73	19	3.4	576	9	AQ724199
C 74	19	3.4	577	7	CV052069
C 75	19	3.4	583	7	CN774204
C 76	19	3.4	587	7	CNS70332
C 77	19	3.4	591	8	DN812679
C 78	19	3.4	597	9	BH269965
C 79	19	3.4	600	7	CNS57111
C 80	19	3.4	603	9	BZ295130
C 81	19	3.4	610	7	CN777760
C 82	19	3.4	618	6	CB555687
C 83	19	3.4	625	8	DN636458
C 84	19	3.4	629	3	BI507057
C 85	19	3.4	638	7	CN276071
C 86	19	3.4	639	7	CNS70542
C 87	19	3.4	646	8	CX024391
C 88	19	3.4	648	7	CR790604
C 89	19	3.4	653	9	BH282880
C 90	19	3.4	654	10	CM105986
C 91	19	3.4	659	6	CA257783
C 92	19	3.4	659	10	BM184039
C 93	19	3.4	663	8	DN242601
C 94	19	3.4	676	9	BZ038035
C 95	19	3.4	676	9	BZ038035

CL347309	RPI14_27
DT014681	VV1091D02
AF062715	AF062715
A1110607	HA0033_Hu
AG594544	Mus muscu
B2717132	PUCGG02TD
CC855478	NDL_36C7
CB58744	ACBNCOURT
BH770411	LIMCARG18
CN351365	170005321
BI033292	PM2-NN008
BI315574	BAF74B08
BX501946	DKEF2079P
BE695762	QV0-CT022
CO174612	NDL_45_D
BI123660	1026P75P
AL911633	AL911633
BM024201	f47d411.x
BI534176	f47d411.x
AM466723	f198E09.x
CNS71020	fag50H06
C2810619	OC_Ba018
AM566806	fR19e02.y
BI880748	fm79D03.x
AV412280	AV412280
BI534292	f188H03.x
BG729141	fp05e04.x
AA148431	z607J02.x
BQ628382	BAD46C07
CR792402	DKEF20690
BI428905	f693A11.x
CD860340	TE_002C14
A1588145	fp96g03.x
BI706193	f402e05.y
CW411105	f6bd001f1
AM527707	UI-R-BT1
CR536667	DKEF20459C
CNS32415	f6f17d06
CU915556	OA_Aba001
BY479743	BY479743
AM154791	f132H02.x
CR774267	DKEF20459L
BE941710	EST421289
BI706265	f403e05.y
AL911634	AL911634
CN492456	MGf*2013f
AQ245104	HS_2059_A
CNS23288	ta05C04
CAB15328	CA12R1203
CNS15164	170005316
CNS51367	170004245
AQ724199	HS_2102_A
CV052069	EST_11517
CN774204	taf59e07
CNS70332	ta93B07
DN812679	ACAC-aac4
BH269965	CA230-6M1
CNS57111	tae40g12
BZ295130	CG1309.r1
CN777760	tae48a05
CB555687	MMSPP0048
DN636458	ACAC-aab4
BI507057	BH170022B
CN276071	170006001
CNS70542	ta93B07
CX024391	Md1v-405
CR790604	DKEF20459M
BH282880	CH230-128
CM105986	104_475_1
CA257783	SCCFL110
BM184039	Danio rer
DN242601	ACAD-aab0
BZ038035	ceh88a07

C 96	19	3.4	677	11	CR310171	mtei-3111	C 169	18	3.2	306	6	CB075944	CB075944 qR8ef06.b
C 97	19	3.4	681	9	AQ287877	nbxb0031d	C 170	18	3.2	307	7	A0067615	A0067615 HS 2238.B
C 98	19	3.4	688	6	CA266323	SCAGJB204	C 171	18	3.2	317	1	AA744366	AA744366 ny51801.78
C 99	19	3.4	688	9	BH930813	od165e11.	C 172	18	3.2	318	6	CD552314	CD552314 B0340H12-
C 100	19	3.4	698	10	CE722100	cl1gr-g88-	C 173	18	3.2	320	10	AG196104	AG196104 Pan tlog1
C 101	19	3.4	699	3	BI967289	BI967289 GM830001A	C 174	18	3.2	321	10	CEB34475	CEB34475 l1gr-g88-
C 102	19	3.4	710	7	CN351363	170005321	C 175	18	3.2	329	6	CA995503	CA995503 r930b12.y
C 103	19	3.4	713	7	CV195898	CGF100344	C 176	18	3.2	329	8	CX569827	CX569827 RVL888.MA
C 104	19	3.4	724	1	AI725481	BNLGH1122	C 177	18	3.2	337	8	L13819	L13819 HMDH13F01
C 105	19	3.4	728	10	AG556836	Mus muscu	C 178	18	3.2	339	6	CB119911	CB119911 K-EST016
C 106	19	3.4	729	8	DT041816	Mdtdp1010	C 179	18	3.2	345	7	CR451235	CR451235
C 107	19	3.4	732	10	AG501209	AG501209 Mus muscu	C 180	18	3.2	347	6	CB120667	CB120667 K-EST0167
C 108	19	3.4	733	10	CW528169	CW528169 OP_Ba002	C 181	18	3.2	350	1	AU233831	AU233831
C 109	19	3.4	737	11	AG418425	Mus muscu	C 182	18	3.2	353	8	T00248	T00248
C 110	19	3.4	738	11	CR826277	GR0AA57D	C 183	18	3.2	353	10	C2645374	C2645374 OM_Ba019
C 111	19	3.4	739	10	CE724554	CC344706 P0HRC477B	C 184	18	3.2	354	1	AU278232	AU278232
C 112	19	3.4	740	9	CC364706	AG490779	C 185	18	3.2	359	8	T23676	T23676 Beq312 N-D4
C 113	19	3.4	750	10	AG490779	AG490779 Mus muscu	C 186	18	3.2	370	1	A1038592	A1038592 ox34e05.8
C 114	19	3.4	762	7	CV195412	CV195412 CGF100343	C 187	18	3.2	370	2	BG735574	BG735574 rK41806.y
C 115	19	3.4	765	7	CV565071	CV565071 ea71c02.	C 188	18	3.2	370	2	BE669385	BE669385 dc58f05.y
C 116	19	3.4	771	2	BG707512	BG707512 602670751	C 189	18	3.2	371	8	R60603	R60603 yhl4b03.y1
C 117	19	3.4	786	7	CV194625	CV194625 CGF100334	C 190	18	3.2	376	2	BG187396	BG187396 RST6387.A
C 118	19	3.4	789	7	CV196340	CV196340 CGF100349	C 191	18	3.2	378	5	BU947116	BU947116 r1f19f03.y
C 119	19	3.4	790	7	CV197687	CV197687 CGF100395	C 192	18	3.2	380	7	CN571335	CN571335 tag50h06.
C 120	19	3.4	795	6	CF445491	CF445491 EST681836	C 193	18	3.2	383	6	CA996221	CA996221 r936c12.y
C 121	19	3.4	797	10	CL829921	CL829921 OR_CBA005	C 194	18	3.2	386	9	CC890518	CC890518 ZMMBRC050
C 122	19	3.4	799	8	CX667260	CX667260 UCRCP01.0	C 195	18	3.2	389	8	T00246	T00246 WEST00967.E
C 123	19	3.4	813	7	CV198649	CV198649 CGF100357	C 196	18	3.2	390	7	CY368381	CY368381 PM2-CT080
C 124	19	3.4	814	1	AU133446	AU133446	C 197	18	3.2	391	1	AM588965	AM588965 ra07e05.y
C 125	19	3.4	817	7	CV198123	CV198123 CGF100396	C 198	18	3.2	391	9	BZ894063	BZ894063 UP_366-21
C 126	19	3.4	821	9	BZ124165	BZ124165 CH230-451	C 199	18	3.2	394	3	BP580911	BP580911 BP580911
C 127	19	3.4	825	7	CV198003	CV198003 CGF100395	C 200	18	3.2	395	11	CR876482	CR876482 Sus scrofa
C 128	19	3.4	829	6	CAB15434	CAL2E1203	C 201	18	3.2	399	1	AV812241	AV812241 AV812241
C 129	19	3.4	830	10	CZ205599	CZ205599 A1AA-aag5	C 202	18	3.2	401	8	DA7180	DA7180 R1G312351A
C 130	19	3.4	837	10	CL654647	CL654647 PRI0121A_	C 203	18	3.2	401	2	BG379700	BG379700 UI-R-CS0-
C 131	19	3.4	855	3	BI600685	BI600685 603247574	C 204	18	3.2	401	10	CM470659	CM470659 f6db001f2
C 132	19	3.4	870	5	BQ425754	BQ425754 AGENCOURT	C 205	18	3.2	403	10	CM111224	CM111224 104.484.1-
C 133	19	3.4	875	8	CX703844	CX703844 gmrtdn80	C 206	18	3.2	405	1	AV819351	AV819351 AV819351
C 134	19	3.4	876	5	CV196635	CV196635 CGF100350	C 207	18	3.2	408	7	CF890289	CF890289 TCTR-1092
C 135	19	3.4	879	5	BO705428	BO705428 Y1A20H04-	C 208	18	3.2	410	7	CNS70245	CNS70245 tag5c04.
C 136	19	3.4	883	5	BQ883066	BQ883066 AGENCOURT	C 209	18	3.2	410	7	BH042103	BH042103 RPT-24-3
C 137	19	3.4	886	5	BQ718140	BQ718140 AGENCOURT	C 210	18	3.2	411	6	CF803846	CF803846 r97b06.y
C 138	19	3.4	909	7	CV197162	CV197162 CGF100350	C 211	18	3.2	412	1	AV810199	AV810199 AV810199
C 139	19	3.4	911	7	CV198398	CV198398 CGF100397	C 212	18	3.2	412	9	BH213420	BH213420 SALK.0091
C 140	19	3.4	926	10	CW950975	CW950975 TGB36.2.C	C 213	18	3.2	413	8	H12973	H12973 y169q10.y1
C 141	19	3.4	926	10	CL735987	CL735987 OR_BBa006	C 214	18	3.2	414	3	BP784170	BP784170 BP784170
C 142	19	3.4	942	7	CN019679	CN019679 AGENCOURT	C 215	18	3.2	415	5	BX840137	BX840137 BX840137
C 143	19	3.4	947	7	CNS11269	CNS11269 AGENCOURT	C 216	18	3.2	420	1	AV520444	AV520444 AV520444
C 144	19	3.4	1007	3	BO057812	BO057812 AGENCOURT	C 217	18	3.2	424	9	AQ304675	AQ304675 HS 2139.A
C 145	19	3.4	1060	3	BM910627	BM910627 AGENCOURT	C 218	18	3.2	425	8	R60616	R60616 yhl4d03.y1
C 146	19	3.4	1097	5	BO717484	BO717484 AGENCOURT	C 219	18	3.2	426	1	AV810239	AV810239 AV810239
C 147	19	3.4	1121	3	BM478977	BM478977 AGENCOURT	C 220	18	3.2	430	1	AV796680	AV796680 AV796680
C 148	19	3.4	1135	9	CC239784	CC239784 CH261-81N	C 221	18	3.2	430	3	BP616213	BP616213 BP616213
C 149	19	3.4	1260	10	AG448708	AG448708 Mus muscu	C 222	18	3.2	430	6	CB121971	CB121971 K-EST0169
C 150	19	3.4	1358	10	AY402220	AY402220 Pan tlog1	C 223	18	3.2	432	1	AM735573	AM735573 r221h09.y
C 151	19	3.4	1365	10	AY402219	AY402219 Homo sapi	C 224	18	3.2	433	9	AQ036363	AQ036363 CIT-HSP-2
C 152	19	3.4	1527	4	CR860890	CR860890 Pongo pyg	C 225	18	3.2	435	1	AV794871	AV794871 AV794871
C 153	19	3.4	1533	4	CR859011	CR859011 Pongo pyg	C 226	18	3.2	436	7	CE971057	CE971057 AUB-1fHrc
C 154	19	3.4	1544	4	CR859512	CR859512 Pongo pyg	C 227	18	3.2	438	3	BU134348	BU134348 BU134348
C 155	19	3.4	1554	4	CR857812	CR857812 Pongo pyg	C 228	18	3.2	438	3	BP616890	BP616890 BP616890
C 156	19	3.4	1566	4	AF149543	AF149543	C 229	18	3.2	438	9	BH122858	BH122858 RPT-24-3
C 157	18	3.2	128	6	CF696620	CF696620 CCAHRK49TF	C 230	18	3.2	439	9	AQ226837	AQ226837 HS 2016.B
C 158	18	3.2	203	7	CK693599	CK693599 SGP1.53689	C 231	18	3.2	439	9	BZ523548	BZ523548 BOKAB13R
C 159	18	3.2	221	1	AM530561	AM530561 UI-R-BT1-	C 232	18	3.2	442	6	CF803891	CF803891 r976f10.y
C 160	18	3.2	244	1	AV242270	AV242270	C 233	18	3.2	445	5	BP612126	BP612126 BP612126
C 161	18	3.2	256	3	BP715548	BP715548	C 234	18	3.2	445	9	AZ598764	AZ598764 IM0413D14
C 162	18	3.2	259	6	CB333333	CB333333 PY343e06.y	C 235	18	3.2	451	10	CM480904	CM480904 f6db001f2
C 163	18	3.2	271	1	AI474789	AI474789 C536e11.x	C 236	18	3.2	451	10	CM480905	CM480905 f6db001f2
C 164	18	3.2	271	3	BJ009744	BJ009744	C 237	18	3.2	452	6	CA673959	CA673959 w18u2.DK0
C 165	18	3.2	287	3	AZ886797	RPT-23-1	C 238	18	3.2	453	3	AI391514	AI391514 r903d12.x
C 166	18	3.2	299	3	BP678541	BP678541	C 239	18	3.2	453	8	H08955	H08955 y193g04.x1
C 167	18	3.2	300	1	AV183805	AV183805	C 240	18	3.2	455	2	BF599851	BF599851 264184.MA
C 168	18	3.2	300	5	C32746	C32746 YUj1	C 241	18	3.2	456	3	BP615409	BP615409 BP615409

242	18	3.2	460	8	D47858	D47858	RICG13586A	315	18	3.2	572	3	BI701634	BI701634	sa118b12.
243	18	3.2	461	5	B0625858	B0625858	ph93909.Y	316	18	3.2	572	3	BU727366	BU727366	BU727366
244	18	3.2	461	6	CA073251	CA073251	SCBPAM105	317	18	3.2	572	3	BP275298	BP275298	BP275298
245	18	3.2	461	6	CAS23919	CAS23919	KS12030C1	318	18	3.2	576	10	CM294028	CM294028	104_774-1
246	18	3.2	462	6	CD811731	CD811731	BN10..001K	319	18	3.2	578	3	BJ491121	BJ491121	BJ491121
247	18	3.2	462	8	N96690	N96690	21493 CD4-1	320	18	3.2	579	3	BU000793	BU000793	BU000793
248	18	3.2	463	10	CE292629	CE292629	t1gr-g88-	321	18	3.2	579	10	CM842298	CM842298	ET12221.D
249	18	3.2	466	2	BE899890	BE899890	181560.MA	322	18	3.2	580	9	A2461686	A2461686	1M0267109
250	18	3.2	467	5	BQ626319	BQ626319	ph96d09.Y	323	18	3.2	581	3	BP255824	BP255824	BP255824
251	18	3.2	468	5	A2310422	A2310422	1M0025E21	324	18	3.2	582	10	CZ100194	CZ100194	OM_Ba010
252	18	3.2	468	7	CF899684	CF899684	A0306B07-	325	18	3.2	585	9	BH824272	BH824272	BACFP20-C
253	18	3.2	480	8	R16271	R16271	ya48c08..r1	326	18	3.2	588	3	BJ082443	BJ082443	CA182443
254	18	3.2	488	3	BQ345320	BQ345320	RC5-NT026	327	18	3.2	588	6	CA121649	CA121649	SERZLR105
255	18	3.2	492	10	CF474439	CF474439	t1gr-g88-	328	18	3.2	589	6	CB439180	CB439180	CV910725
256	18	3.2	501	2	BF251598	BF251598	EST418947	329	18	3.2	589	9	A2910725	A2910725	RCPI-24-1
257	18	3.2	502	3	BI538205	BI538205	428640.MA	330	18	3.2	591	1	AV984026	AV984026	AV984026
258	18	3.2	504	6	CA870707	CA870707	K0904D09-	331	18	3.2	591	7	CV219733	CV219733	EST879443
259	18	3.2	505	6	CA903113	CA903113	PCS02549F	332	18	3.2	593	11	CPA562683	CPA562683	
260	18	3.2	509	2	BF044692	BF044692	BP250010A	333	18	3.2	595	6	CB439180	CB439180	668791.MA
261	18	3.2	509	6	CD843182	CD843182	RCQ2.130N	334	18	3.2	596	8	DN489075	DN489075	S075F04.3
262	18	3.2	510	3	BU733550	BU733550	BU733550	335	18	3.2	597	8	CV977041	CV977041	UWC-Dc1.0
263	18	3.2	511	3	BU733551	BU733551	BU733551	336	18	3.2	599	5	BU042582	BU042582	PP_LBd001
264	18	3.2	511	6	CD822333	CD822333	BM25..044N	337	18	3.2	601	9	A2446686	A2446686	1M0243P07
265	18	3.2	512	10	CM294029	CM294029	104_774-1	338	18	3.2	602	6	CA696004	CA696004	w1mk8.pko
266	18	3.2	513	7	CF980072	CF980072	Y8B4F06.Y	339	18	3.2	602	11	DB060596	DB060596	CrypOsgpO
267	18	3.2	514	1	AU221830	AU221830	AU221830	340	18	3.2	604	9	BH037123	BH037123	RCPI-24-3
268	18	3.2	516	6	CD817719	CD817719	BM20..042O	341	18	3.2	607	1	AV957316	AV957316	AV957316
269	18	3.2	517	1	AM034566	AM034566	AM034566	342	18	3.2	610	6	CB527733	CB527733	UI-M-PY0-
270	18	3.2	518	6	CB438817	CB438817	6877711.MA	343	18	3.2	615	6	CD816121	CD816121	BM15..028J
271	18	3.2	519	1	AI391951	AI391951	486005H04	344	18	3.2	617	3	BJ310536	BJ310536	BM150536
272	18	3.2	523	9	AZ967344	AZ967344	2M0238D14	345	18	3.2	619	1	AU212088	AU212088	AU212088
273	18	3.2	524	2	BB703898	BB703898	BB703898	346	18	3.2	619	9	AZ511729	AZ511729	RCPI-11-8
274	18	3.2	525	1	AA605392	AA605392	30428.Lam	347	18	3.2	619	10	C2100500	C2100500	OM_Ba010
275	18	3.2	528	3	BI510714	BI510714	BB160003A	348	18	3.2	620	7	CV219734	CV219734	602594589
276	18	3.2	529	7	CO877190	CO877190	BoyGen_05	349	18	3.2	620	2	BF024176	BF024176	PvP_513.L
277	18	3.2	532	1	AM618525	AM618525	EST320511	350	18	3.2	627	2	BB662275	BB662275	BB662275
278	18	3.2	533	3	BU008103	BU008103	BU008103	351	18	3.2	628	10	C2497483	C2497483	OA_BBa014
279	18	3.2	534	3	BU009383	BU009383	BU009383	352	18	3.2	629	3	BF298723	BF298723	020PB812
280	18	3.2	534	7	CK744146	CK744146	eca01-3c8	353	18	3.2	629	2	BJ131181	BJ131181	BJ131181
281	18	3.2	535	9	AO223808	AO223808	HS_2218.A	354	18	3.2	632	9	CD817335	CD817335	BM20..041I
282	18	3.2	536	2	BE106088	BE106088	UI-R-BOT-	355	18	3.2	632	6	CD817718	CD817718	BM20..047E
283	18	3.2	537	3	BJ524169	BJ524169	BJ524169	356	18	3.2	633	6	CD820120	CD820120	BM20..051E
284	18	3.2	537	7	CF825866	CF825866	EST703248	357	18	3.2	631	6	BJ031963	BJ031963	BM20..051E
285	18	3.2	538	7	CK893627	CK893627	SGP153719	358	18	3.2	633	2	BG181278	BG181278	RCST4.Alche
286	18	3.2	539	2	BF039887	BF039887	BP250025A	359	18	3.2	639	1	AV997156	AV997156	AV997156
287	18	3.2	539	2	BF045364	BF045364	BP250025A	360	18	3.2	639	3	B0095480	B0095480	KK05907.Y
288	18	3.2	539	3	BI471522	BI471522	88G21e02.	361	18	3.2	639	6	CD818923	CD818923	BM20..047E
289	18	3.2	540	3	BU732047	BU732047	BU732047	362	18	3.2	639	6	CD818923	CD818923	BM20..047E
290	18	3.2	543	9	B25973	B25973	T3A4TF.TAMU	363	18	3.2	640	2	BB427379	BB427379	PSR6369-B
291	18	3.2	543	9	CC133762	CC133762	NDL_71F22	364	18	3.2	641	9	BH824780	BH824780	BACP21-C
292	18	3.2	544	2	BF044189	BF044189	BP250012B	365	18	3.2	643	2	BB661935	BB661935	BB661935
293	18	3.2	544	6	CAS19703	CAS19703	KS1002980	366	18	3.2	644	1	AU238553	AU238553	AU238553
294	18	3.2	544	6	CAS19703	CAS19703	KS1002980	367	18	3.2	644	3	BJ391498	BJ391498	BJ391498
295	18	3.2	545	10	CM493595	CM493595	feb0001f2	368	18	3.2	644	11	CPA562060	CPA562060	
296	18	3.2	546	6	CF303078	CF303078	ASFP1--01-	369	18	3.2	645	10	CE389744	CE389744	
297	18	3.2	549	3	BU009214	BU009214	BU009214	370	18	3.2	646	1	AU212632	AU212632	AU212632
298	18	3.2	549	7	CO551383	CO551383	LYEST9862	371	18	3.2	646	6	CA240976	CA240976	SCUTFL307
299	18	3.2	550	6	CB423606	CB423606	597065.MA	372	18	3.2	646	6	CD818920	CD818920	BM20..044O
300	18	3.2	550	6	AZ619876	AZ619876	1M0452P18	373	18	3.2	647	3	CD817180	CD817180	BM20..044O
301	18	3.2	551	3	BM654648	BM654648	K-EST0137	374	18	3.2	648	6	CD812327	CD812327	BM20..044O
302	18	3.2	551	7	CO884423	CO884423	BOvGen_12	375	18	3.2	648	10	AG034328	AG034328	Pan_t1c0g1
303	18	3.2	556	1	AI769648	AI769648	w125c01.x	376	18	3.2	650	1	AU211923	AU211923	AU211923
304	18	3.2	556	1	AA460718	AA460718	zkx6901..8	377	18	3.2	650	3	BJ795593	BJ795593	BJ795593
305	18	3.2	556	9	AO127273	AO127273	HS_3053.B	378	18	3.2	650	8	DR004737	DR004737	TC117586
306	18	3.2	558	1	AV954654	AV954654	AV954654	379	18	3.2	652	3	BM663133	BM663133	UI-M-E00-
307	18	3.2	558	2	BE683086	BE683086	181561.MA	380	18	3.2	653	6	CD888947	CD888947	G118..110J
308	18	3.2	558	11	CR340401	CR340401	mtc4-72E2	381	18	3.2	654	7	CN033855	CN033855	Match_6.L1
309	18	3.2	559	1	AU219818	AU219818	AU219818	382	18	3.2	654	10	CM168505	CM168505	104_578-1
310	18	3.2	561	1	AV957477	AV957477	AV957477	383	18	3.2	654	10	CE539377	CE539377	t1gr-g88-
311	18	3.2	563	6	CD818845	CD818845	BM20..047A	384	18	3.2	655	6	CD905731	CD905731	G468..102L
312	18	3.2	563	1	AU215224	AU215224	AU215224	385	18	3.2	657	1	AJ732606	AJ732606	AJ732606
313	18	3.2	569	9	AO524493	AO524493	HS_5214.B	386	18	3.2	657	7	CK468638	CK468638	AMP129.CO
314	18	3.2	571	9	AO283376	AO283376	RCIT11-69	387	18	3.2	658	5	BM346197	BM346197	BM346197

388	18	3.2	659	1	AU211804	AU211804	461	18	3.2	724	10	CM029105	CM029105 104_256.1
389	18	3.2	659	10	CE83990	CE83990 tigr-g88-	462	18	3.2	725	2	BG212803	BG212803 RST32398
390	18	3.2	660	6	CD819000	CD819000 BN20_0471	463	18	3.2	725	5	BU939588	BU939588 AGENCOURT
391	18	3.2	660	10	CE377546	CE377546 tigr-g88-	464	18	3.2	725	10	AG604537	AG604537 Mus muscu
392	18	3.2	663	6	CF306223	CF306223 HDAL--03-	465	18	3.2	725	10	AG604537	AG604537 F99_F08.S
393	18	3.2	663	6	CF310784	CF310784 ABE--05-K	466	18	3.2	727	6	BI543885	BI543885 BN25_053N
394	18	3.2	664	3	BU818031	BU818031 BU775322	467	18	3.2	729	6	BZ446527	BZ446527 BONPK38TF
395	18	3.2	665	3	BU775322	BU775322 BU775322	468	18	3.2	730	1	AI041834	AI041834 OY34C03.X
396	18	3.2	665	3	BU812311	BU812311 BU812311	469	18	3.2	730	7	CO024064	CO024064 EST789197
397	18	3.2	665	8	CE835728	CE835728 ACAC-aa6	470	18	3.2	731	6	CD872203	CD872203 AZO2_120F
398	18	3.2	665	10	CM588841	CM588841 OA_ABA012	471	18	3.2	731	6	CK776799	CK776799 968165.MA
399	18	3.2	667	3	BU659051	BU659051 BU659051	472	18	3.2	733	6	CD642113	CD642113 AGENCOURT
400	18	3.2	668	3	BU792186	BU792186 BU792186	473	18	3.2	735	7	CO428906	CO428906 UI-M-HXO-
401	18	3.2	668	5	BM252739	BM252739 BM252739	474	18	3.2	738	10	CL766270	CL766270 OR_BA013
402	18	3.2	668	10	CG913896	CG913896 ZMMB037	475	18	3.2	739	6	CB457471	CB457471 714824.MA
403	18	3.2	669	2	BB616518	BB616518 BB616518	476	18	3.2	740	3	BQ042226	BQ042226 UI-M-EQO-
404	18	3.2	670	3	BU817001	BU817001 BU817001	477	18	3.2	743	10	CM578350	CM578350 OA_ABA010
405	18	3.2	670	6	CA192791	CA192791 SCRLSB104	478	18	3.2	743	10	AG539867	AG539867 Mus muscu
406	18	3.2	670	6	BM034334	BM034334 BM034334	479	18	3.2	744	3	BU791431	BU791431 BX320222
407	18	3.2	672	9	BZ433550	BZ433550 id50612.9	480	18	3.2	744	10	BX230222	BX230222 Danto_rer
408	18	3.2	674	7	CM033854	CM033854 Math_6.11	481	18	3.2	745	2	BE541824	BE541824 601064102
409	18	3.2	677	10	CE765462	CE765462 tigr-g88-	482	18	3.2	745	3	BU794380	BU794380 BU794380
410	18	3.2	678	3	BU798362	BU798362 BU798362	483	18	3.2	745	3	BU810700	BU810700 BU810700
411	18	3.2	680	3	BU778047	BU778047 BU778047	484	18	3.2	745	5	BU216935	BU216935 603755473
412	18	3.2	680	8	DN816430	DN816430 ACAC-aab9	485	18	3.2	747	3	BU810098	BU810098 BU810098
413	18	3.2	682	3	BU784337	BU784337 BU784337	486	18	3.2	747	6	CD351031	CD351031 UI-M-GIO-
414	18	3.2	685	3	CD817887	CD817887 BN20_0431	487	18	3.2	747	7	CK639942	CK639942 UI-M-HNO-
415	18	3.2	685	8	CK434576	CK434576 JGI_XZG17	488	18	3.2	747	10	CM831094	CM831094 OP_BA008
416	18	3.2	686	1	AV982799	AV982799 AV982799	489	18	3.2	748	5	BM043930	BM043930 BM043930
417	18	3.2	686	6	CF726349	CF726349 UI-M-HBO-	490	18	3.2	751	10	CM606523	CM606523 OA_ABA014
418	18	3.2	687	6	CM183193	CM183193 104_599.1	491	18	3.2	752	6	CB653019	CB653019 OSJNEC03K
419	18	3.2	687	6	CF306358	CF306358 HDAL--03-	492	18	3.2	752	6	BH184801	BH184801 026_M_05-
420	18	3.2	689	6	CE834482	CE834482 ACAC-aa3	493	18	3.2	752	11	CM556236	CM556236 OA_ABA007
421	18	3.2	689	10	AC056487	AC056487 Pan_trog1	494	18	3.2	752	11	CM507060	CM507060 T3_end of
422	18	3.2	689	10	AG056487	AG056487 Pan_trog1	495	18	3.2	754	6	CF825942	CF825942 EST70324
423	18	3.2	690	2	BG440198	BG440198 GA_BA000	496	18	3.2	755	3	BU128370	BU128370 BU128370
424	18	3.2	691	10	CM473221	CM473221 fdbb001f2	497	18	3.2	755	6	CF713276	CF713276 CCAG49TF
425	18	3.2	693	5	BX100014	BX100014 BU216464	498	18	3.2	755	3	CV203057	CV203057 EST662767
426	18	3.2	694	1	AU216464	AU216464 AU216464	499	18	3.2	756	3	BM160936	BM160936 EST653459
427	18	3.2	696	10	CE371987	CE371987 tigr-g88-	500	18	3.2	758	1	AV405557	AV405557 AV405557
428	18	3.2	696	6	CD861812	CD861812 AZO1_0030	501	18	3.2	758	9	BH484031	BH484031 BQGPW95TR
429	18	3.2	696	6	CK835713	CK835713 ACAC-aa1	502	18	3.2	761	3	BU784496	BU784496 BU784496
430	18	3.2	696	9	BZ020853	BZ020853 ce113d01.	503	18	3.2	761	10	CE655969	CE655969 tigr-g88-
431	18	3.2	696	11	CR478545	CR478545 ce113d01.	504	18	3.2	762	10	CM493396	CM493396 fdbb001f2
432	18	3.2	697	1	AI612522	AI612522 TBMG0332	505	18	3.2	764	7	CN283197	CN283197 170005338
433	18	3.2	698	1	CE0872302	CE0872302 AZO2_120F	506	18	3.2	764	7	CO023862	CO023862 RST788995
434	18	3.2	698	3	BI934721	BI934721 BST554610	507	18	3.2	768	9	AZ238066	AZ238066 RPC1-23-3
435	18	3.2	698	3	BU142551	BU142551 BU142551	508	18	3.2	776	1	AU732612	AU732612 AU732612
436	18	3.2	699	7	CO048271	CO048271 LT_PAHCF	509	18	3.2	781	7	CR280432	CR280432 CR280432
437	18	3.2	700	10	CE356566	CE356566 tigr-g88-	510	18	3.2	782	6	CF822598	CF822598 EST699980
438	18	3.2	704	6	CE434846	CE434846 BST671191	511	18	3.2	784	7	CO918205	CO918205 AGENCOURT
439	18	3.2	704	8	CK633154	CK633154 taji39g04.	512	18	3.2	785	3	BU780244	BU780244 BU780244
440	18	3.2	704	10	CM276852	CM276852 104_750.1	513	18	3.2	786	7	CO429772	CO429772 UI-M-HXO-
441	18	3.2	707	10	CM175990	CM175990 104_588.1	514	18	3.2	788	8	CK459162	CK459162 JGI_XZG27
442	18	3.2	707	8	DM597590	DM597590 OA_ABA016	515	18	3.2	788	10	CE263926	CE263926 OM_BA017
443	18	3.2	708	10	DR597590	DR597590 BST987718	516	18	3.2	791	10	AY413237	AY413237 Mus muscu
444	18	3.2	709	11	AZ955156	AZ955156 2M0231G10	517	18	3.2	794	8	CK340122	CK340122 JGI_XZT61
445	18	3.2	709	11	CR876426	CR876426 Sns_scof	518	18	3.2	795	8	CK435796	CK435796 JGI_XZT61
446	18	3.2	712	11	DE108065	DE108065 Oryzias	519	18	3.2	796	3	BU798577	BU798577 BU798577
447	18	3.2	713	4	CNS09A2	BN049755 Single re	520	18	3.2	796	9	CC562052	CC562052 CH240_472
448	18	3.2	714	7	CN215218	CN215218 28996.Sus	521	18	3.2	797	3	BU815300	BU815300 BU815300
449	18	3.2	715	9	CE024682	CE024682 tigr-g88-	522	18	3.2	797	7	CK636274	CK636274 UI-M-HNO-
450	18	3.2	715	8	CV842041	CV842041 ID0ADD3AB	523	18	3.2	798	3	BU793602	BU793602 BU793602
451	18	3.2	715	10	CM029106	CM029106 104_256.1	524	18	3.2	799	3	BU792945	BU792945 BU792945
452	18	3.2	716	1	AU216809	AU216809 AU216809	525	18	3.2	800	3	BU740322	BU740322 BU740322
453	18	3.2	717	3	BU150193	BU150193 AG338166 Mus muscu	526	18	3.2	800	3	BU784898	BU784898 BU784898
454	18	3.2	719	8	DT063849	DT063849 AGENCOURT	527	18	3.2	801	7	CO013857	CO013857 BJA813168
455	18	3.2	720	5	CD639586	CD639586 AGENCOURT	528	18	3.2	801	7	CO013857	CO013857 BJA813168
456	18	3.2	721	5	BU442353	BU442353 603019167	529	18	3.2	803	10	CG812272	CG812272 FSAJ15TF
457	18	3.2	721	5	BM313478	BM313478 BM313478	530	18	3.2	805	3	BU776077	BU776077 BU776077
458	18	3.2	723	5	CF824965	CF824965 EST702347	531	18	3.2	806	6	CD492925	CD492925 CDA02-C04
459	18	3.2	723	6	CD823726	CD823726 BN25_049M	532	18	3.2	806	7	CO008099	CO008099 EST796434
460	18	3.2	724	6	CD823726	CD823726 BN25_049M	533	18	3.2	807	8	CX973557	CX973557 JGI_CAA08

534	18	3.2	810	9	CC714169	CC714169 OGBS29TH	C 607	18	3.2	930	10	AY407285	AY407285 Mus muscu
535	18	3.2	813	6	CF820850	EST698232	C 608	18	3.2	931	7	CV210691	CV210691 EST870401
536	18	3.2	814	6	CF822296	EST699678	C 609	18	3.2	932	5	BY709303	BY709303 Mus muscu
537	18	3.2	814	8	CX633355	ta139e01.	C 610	18	3.2	935	6	CF825901	CF825901 EST703283
538	18	3.2	814	8	DR852902	JGI_CABG8	C 611	18	3.2	937	7	CO007844	CO007844 EST796179
539	18	3.2	815	7	CO024715	EST803099	C 612	18	3.2	941	7	CV203058	CV203058 EST862768
540	18	3.2	815	8	DR429428	max16906.	C 613	18	3.2	943	7	CR852984	CR852984 CR852984
541	18	3.2	816	6	CF827108	EST704490	C 614	18	3.2	944	4	CNS08BME	BX008370 Single re
542	18	3.2	817	6	CF823740	EST701122	C 615	18	3.2	945	10	CM639189	CM639189 OA_Aba017
543	18	3.2	817	10	DU082163	277423 To	C 616	18	3.2	958	7	CV210692	CV210692 EST870402
544	18	3.2	818	10	CG845436	CG84A54TH	C 617	18	3.2	959	1	AI525673	AI525673 prt. 3. 04
545	18	3.2	817	10	DU086099	37743 Tom	C 618	18	3.2	963	11	CNS03Y75	AI525696 Tetradodon
546	18	3.2	820	6	CB558329	AGENCOURT	C 619	18	3.2	971	6	CF822880	CF822880 EST700262
547	18	3.2	822	3	BI771392	603059413	C 620	18	3.2	972	4	CNS08BMD	BX008369 Single re
548	18	3.2	822	10	CM713147	AI1A-aa8	C 621	18	3.2	974	10	CNS02GTC	AL0051269 Tetradodon
549	18	3.2	823	8	CX968690	JGI_CAP3	C 622	18	3.2	976	10	CNS004CM	AL0051269 Tetradodon
550	18	3.2	824	8	CX381997	JGI_XZT53	C 623	18	3.2	983	6	CF823666	CF823666 EST8070048
551	18	3.2	825	7	CO013974	EST802309	C 624	18	3.2	986	7	CV203056	CV203056 EST8627766
552	18	3.2	825	10	DU070491	138260 To	C 625	18	3.2	987	10	CG966936	CG966936 166028 To
553	18	3.2	826	8	CV770532	FGAS06492	C 626	18	3.2	987	10	CL480004	CL480004 SAIL. 316
554	18	3.2	829	7	CO013975	EST802310	C 627	18	3.2	989	10	DU016564	DU016564 239062 To
555	18	3.2	830	7	BU785094	BU785094	C 628	18	3.2	991	11	CNS03KPG	AI248461 Tetradodon
556	18	3.2	831	6	CA493148	AGENCOURT	C 629	18	3.2	994	3	BMS54449	BMS54449 AGENCOURT
557	18	3.2	832	8	CX419339	JGI_XZG13	C 630	18	3.2	995	4	CNS08J5U	BX014254 Single re
558	18	3.2	833	7	CO033529	EST811913	C 631	18	3.2	1012	9	CC780710	CC780710 ZMMBRC043
559	18	3.2	837	6	CF824289	EST701671	C 632	18	3.2	1026	5	BX839817	BX839817 BX839817
560	18	3.2	837	10	BX190492	Dantio Ter	C 633	18	3.2	1036	9	CC206985	CC206985 CH261-180
561	18	3.2	838	5	BU131402	603540512	C 634	18	3.2	1039	10	CG262659	CG262659 109842121
562	18	3.2	838	6	CF825695	EST703077	C 635	18	3.2	1045	10	CG269110	CG269110 169229 To
563	18	3.2	839	2	BE614644	601504586	C 636	18	3.2	1049	3	BQ212075	BQ212075 AGENCOURT
564	18	3.2	840	3	BU782225	BU782225	C 637	18	3.2	1061	10	CG268912	CG268912 168998 To
565	18	3.2	840	2	BE255910	601109880	C 638	18	3.2	1066	9	CC192205	CC192205 CH261-95F
566	18	3.2	841	10	CM712847	AI1A-aa8	C 639	18	3.2	1090	7	CK162840	CK162840 FGAS01544
567	18	3.2	841	10	CG269733	OGWDLITV	C 640	18	3.2	1125	8	DN730715	DN730715 CNBS4-E01
568	18	3.2	842	11	CNS04PWO	AL301833 Tetradodon	C 641	18	3.2	1127	10	CL516284	CL516284 SAIL. 916
569	18	3.2	848	6	CF705535	CF705535 CCABC37TF	C 642	18	3.2	1135	9	CC286602	CC286602 CH261-146
570	18	3.2	850	7	CR572014	CR572014	C 643	18	3.2	1143	9	CC248361	CC248361 CH261-188
571	18	3.2	851	4	CNS08VHT	BX034125 Single re	C 644	18	3.2	1172	9	CC212673	CC212673 CH261-75G
572	18	3.2	851	7	CO015462	EST785844	C 645	18	3.2	1184	9	CC288970	CC288970 CH261-176
573	18	3.2	853	6	CF822379	EST699761	C 646	18	3.2	1195	9	CC246612	CC246612 CH261-157
574	18	3.2	856	9	CC589107	CH240_387	C 647	18	3.2	1201	1	AJ928237	AJ928237 AJ928237
575	18	3.2	858	6	CF824038	EST701420	C 648	18	3.2	1201	10	CNS001CL	AL060206 DrosoPhila
576	18	3.2	863	10	AG855145	AG855145 Oryza sat	C 649	18	3.2	1262	4	AK009644	AK009644 Mus muscu
577	18	3.2	864	4	CNS09179	BX063553 Single re	C 650	18	3.2	1311	10	CL960647	CL960647 ObiFCC004
578	18	3.2	864	10	CM972982	CM972982 AI1A-aa5	C 651	18	3.2	2320	4	CR925989	CR925989 Pongo pyg
579	18	3.2	870	10	CL474589	SAIL_222	C 652	18	3.2	3239	4	AK049458	AK049458 Mus muscu
580	18	3.2	871	10	CM954881	TCB44.3 F	C 653	17	3.0	101	1	AA845079	AA845079 Akb2B01.8
581	18	3.2	873	8	DN074542	JGI_CABDB	C 654	17	3.0	117	2	BI142368	BI142368 949037D05
582	18	3.2	877	3	BU746839	BU746839	C 655	17	3.0	133	8	DN25877	DN25877 HUMCS05524
583	18	3.2	880	6	CF827723	EST705105	C 656	17	3.0	137	8	DN251776	DN251776 ACAB-aa9
584	18	3.2	880	10	CM218116	CM218116 AI1A-aa13	C 657	17	3.0	138	3	BU904374	BU904374 B3904374
585	18	3.2	882	10	CM702636	AI1A-aa2	C 658	17	3.0	142	9	BZ808457	BZ808457 PUPH428TD
586	18	3.2	888	6	CF823400	EST700782	C 659	17	3.0	149	9	BZ372976	BZ372976 1674304.b
587	18	3.2	889	6	CA986313	AGENCOURT	C 660	17	3.0	149	10	AI756877	AI756877 Arabidops
588	18	3.2	892	6	CF827698	EST705080	C 661	17	3.0	151	2	BE485602	BE485602 172687 BA
589	18	3.2	893	6	CF823841	EST701223	C 662	17	3.0	153	2	BE589672	BE589672 naa0807-
590	18	3.2	894	6	CF820891	EST698273	C 663	17	3.0	153	2	BE208353	BE208353 hb5605.x
591	18	3.2	895	9	CC093385	CSU-K34.1	C 664	17	3.0	156	7	CV315357	CV315357 CM1-HT092
592	18	3.2	895	10	CM786635	SP_Ba002	C 665	17	3.0	163	9	AZ775079	AZ775079 ZM0007L01
593	18	3.2	896	5	BU152920	AGENCOURT	C 666	17	3.0	182	2	BB231641	BB231641 BB231641
594	18	3.2	897	10	CM010050	ZMMBLA001	C 667	17	3.0	187	1	AI792028	AI792028 os02E04.y
595	18	3.2	899	10	DU088089	32515 Tom	C 668	17	3.0	192	2	BI003544	BI003544 MX3-HN012
596	18	3.2	904	7	CO012192	EST800527	C 669	17	3.0	195	10	CC029412	CC029412 OM_BA002
597	18	3.2	904	7	CO019709	EST815802	C 670	17	3.0	197	3	BQ038044	BQ038044 pmtc.pko
598	18	3.2	906	6	CF826442	EST703824	C 671	17	3.0	197	2	CM292968	CM292968 104-773.y
599	18	3.2	907	8	CX328614	JGI_XZT67	C 672	17	3.0	199	2	BG409273	BG409273 gb82E10.y
600	18	3.2	911	5	BU912729	AGENCOURT	C 673	17	3.0	199	9	B66104	B66104 CIT-HSP-202
601	18	3.2	916	5	BU071625	AGENCOURT	C 674	17	3.0	212	5	BU890805	BU890805 P04H11.P
602	18	3.2	916	6	CF826289	EST703671	C 675	17	3.0	212	10	CU310643	CU310643 0354741-0
603	18	3.2	918	10	CM251417	GMW2-86C2	C 676	17	3.0	216	8	DN359107	DN359107 LKB3677-0
604	18	3.2	918	11	CNS04H8B	AL90612 Tetradodon	C 677	17	3.0	221	8	H21635	H21635 ytt7H11.t1
605	18	3.2	924	6	CA987658	CA987658 AGENCOURT	C 678	17	3.0	229	7	CN340689	CN340689 170005999
606	18	3.2	930	6	CF827896	EST705278	C 679	17	3.0	230	7	CN340688	CN340688 170006001

680	17	3.0	232	1	A1685520	A1685520 tu36c09.x	C 753	17	3.0	325	9	BH145763	BH145763 TDGPA16TH
681	17	3.0	232	10	CG628093	CG628093 OSR389339	754	17	3.0	327	5	BY114218	BY114218 BY114218
682	17	3.0	234	5	BU099090	BU099090 3524.1.24	755	17	3.0	327	5	BY114396	BY114396 BY114396
683	17	3.0	235	1	AV337574	AV337574 AV337574	756	17	3.0	327	5	BY114609	BY114609 BY114609
684	17	3.0	239	1	AV309300	AV309300 AV309300	757	17	3.0	327	5	BY129616	BY129616 BY329616
685	17	3.0	239	1	BI506735	BI506735 BI170032A	758	17	3.0	328	5	BP942313	BP942313 BP942313
686	17	3.0	239	10	CL908455	CL908455 OA_ABA000	759	17	3.0	329	7	BY790617	BY790617 BY790617
687	17	3.0	241	2	BE768836	BE768836 PM1-FT002	760	17	3.0	329	7	CK099179	CK099179 A055P21.5
688	17	3.0	243	3	BI505363	BI505363 BI170026A	761	17	3.0	330	1	A1014609	A1014609 ou40c05.x
689	17	3.0	243	3	BI505672	BI505672 BI170032A	762	17	3.0	330	5	BY125112	BY125112 BY125112
690	17	3.0	243	3	BI505696	BI505696 BI170030A	763	17	3.0	331	7	CN761183	CN761183 ID0AAA2CE
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693	17	3.0	245	1	AV292974	AV292974 AV292974	766	17	3.0	332	9	CC199627	CC199627 XH754_Bay
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701	17	3.0	258	9	BZ844846	BZ844846 C1gr-g88-	774	17	3.0	339	2	BP448742	BP448742 n6e32e04.x
702	17	3.0	259	3	BJ397492	BJ397492 BJ397492	775	17	3.0	340	8	CX110911	CX110911 E1053K12
703	17	3.0	260	1	AM358117	AM358117 42030 MAR	776	17	3.0	341	5	BY334433	BY334433 BY334433
704	17	3.0	262	10	AG222858	AG222858 Lotu8 cor	777	17	3.0	342	1	A1286095	A1286095 qh99902.x
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707	17	3.0	272	7	CN932335	CN932335 000429A8B	780	17	3.0	345	10	AG979832	AG979832 Drogoph11
708	17	3.0	274	1	AA679177	AA679177 ac57c04.8	781	17	3.0	345	5	AM244673	AM244673 SMOA3KCM
709	17	3.0	275	8	H88902	H88902 yw24g09.x1	782	17	3.0	345	5	BY109136	BY109136 BY109136
710	17	3.0	278	1	BB158134	BB158134 BB158134	783	17	3.0	345	8	DA2931	DA2931 D42931 R1ce
711	17	3.0	281	10	CE2559233	CE2559233 RHAI30 Ba	784	17	3.0	347	7	CV200923	CV200923 km10c04.y
712	17	3.0	281	9	BZ762865	BZ762865 SALK_1092	785	17	3.0	350	9	BZ753582	BZ753582 PUDC347TD
713	17	3.0	284	10	CE778272	CE778272 OSL_Ba013	786	17	3.0	351	10	AG251591	AG251591 Lotu8 cor
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725	17	3.0	298	10	CG551673	CG551673 OST158877	798	17	3.0	361	7	CO728210	CO728210 UMC-bend
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732	17	3.0	308	10	CE728724	CE728724 60352748	805	17	3.0	364	5	BY131660	BY131660 BY131660
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743	17	3.0	315	1	AA939145	AA939145 op63h08.8	816	17	3.0	375	5	BY076096	BY076096 BY076096
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747	17	3.0	319	5	BY114751	BY114751 BY114751	820	17	3.0	377	8	D27951	D27951 CRLK006E4F
748	17	3.0	321	7	BY114047	BY114047 BY114047	821	17	3.0	377	8	RA4256	RA4256 yj01e11.81
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RPC11 Human Male BAC Library"

ORIGIN

Query Match          3.8%; Score 21; DB 9; Length 346;
Best Local Similarity 100.0%; Pident. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173  AAATTATCTTCCAAATPAAA 193
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DB      190  AAATTATCTTCCAAATPAAA 170

RESULT 2
LOCUS      AM069787/c
DEFINITION c510e08.x1 Human bone marrow stromal cells Homo sapiens CDNA clone
ACCESSION  AM069787
VERSION     AM069787.1
KEYWORDS   EST. GI:6024785
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DEFINITION	RPc11-6402.TK RPc1-11 Homo sapiens genomic clone RPc1-11-6402,				
ACCESSION	RPc11-6402.TK RPc1-11 Homo sapiens genomic clone RPc1-11-6402,				
VERSION	AQ237761				
KEYWORDS	AQ237761.1 GI:3670052				
SOURCE	GSS.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.				
TITLE	1 (bases 1 to 346)				
JOURNAL	Adams, M.D., Rounsley, S. D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, D.C.				
COMMENT	Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)				
OTHER	Other GSSs: RPc11-6402.TJ				
CONTACT	Contact: Mark Adams				
DEPARTMENT	Department of Eukaryotic Genomics				
INSTITUTE	The Institute for Genomic Research				
ADDRESS	9712 Medical Center Dr., Rockville, MD 20850, USA				
TEL	Tel: 301 838 0200				
FAX	Fax: 301 838 0208				
EMAIL	Email: mdadams@igr.org				
CLONES	Clones are derived from the human BAC library RPc1-11. For BAC				
LIBRARY	library availability, please contact Pieter de Jong				
PIETERDEJONG	(pieterdejong.med.buffalo.edu). Clones may be purchased from				
BACPAC	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from				
RESEARCH	Research Genetics (info@reagen.com). BAC end search page:				
HTTP	http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html				
SEQ	Seq primer: T7				
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JOURNAL: Genomics 79 (1), 7-17 (2002)
 PUBMED 11827452
 COMMENT Contact: Libin Jia
 Medical Genetics Branch
 National Human Genome Research Institute
 10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
 Tel: 301-402-4877
 Fax: 301-496-7157
 Email: libin@helix.nih.gov
 DNA Sequencing and analyses by National Institutes of Health
 Intramural Sequencing Center (NISC).
 Plate: 50 row: e column: 08
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
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 mRNA made from human bone marrow stroma, cDNA made by
 oligo-dT priming. Directionally cloned. Size-selected for
 average insert size >0.5 kb. Library constructed by Dr.
 Marian Young and Dr. Pamela Gehron Robey (NIDCR). Library
 supplied by Dr. Libin Jia (NHGRI)"

ORIGIN
 Query Match 3.8%; Score 21; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

173 AATTATCTTCGAAATGAAA 193

Db 40 AATATCTCCAAATATAA 20

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RESULT 3
CE052269/c 557 bp DNA linear GSS 24-SEP-2003
LOCUS tigr-gss-dog-17000358213862 Dog library Canis familiaris genomic.
DEFINITION genomic survey sequence.
ACCESSION CE052269
VERSION CE052269.1 GI:35095672
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE
AUTHORS 1 (bases 1 to 557)
Kirnes, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirnes EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirnes@tigr.org
Class: shotgun.

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 AATATCTCCAAATATAA 193
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Db 264 AATATCTCCAAATATAA 244

RESULT 4
BM864686 559 bp mRNA linear EST 24-MAY-2005
LOCUS BM864686
DEFINITION neu84686 Amphioxus Branchiostoma floridae unpublished cDNA library,
neutula whole animal Branchiostoma floridae cDNA clone bne073909
5', mRNA sequence.
ACCESSION BM864686
VERSION BM864686.1 GI:66479363
KEYWORDS EST.
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.

REFERENCE
AUTHORS 1 (bases 1 to 559)
Yu, J., Holland, L.Z., Shin, J.-T., Kohara, Y., Satou, Y. and Satoh, N.
TITLE Expressed genes in Branchiostoma floridae
JOURNAL Unpublished (2005)
COMMENT Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

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source Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 GAAGTAGCTGAAGCTTCACT 288
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Db 505 GAAGTAGCTGAAGCTTCACT 525

RESULT 5
DR421506/c 582 bp mRNA linear EST 29-JUN-2005
LOCUS DR421506
DEFINITION CCHS7E08 Coprinus cinereus heat-shocked mycelia cDNAs Coprinopsis
cinerea cDNA, mRNA sequence.
ACCESSION DR421506
VERSION DR421506.1 GI:68323522
KEYWORDS EST

SOURCE Coprinopsis cinerea (Coprinus cinereus)
ORGANISM Coprinopsis cinerea
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pezizomycotina; Coprinops.
1 (bases 1 to 582)

REFERENCE
AUTHORS Carlson, M.D., Barr, C., Murphy, B., Wilke, S.K., Gathman, A.C.,
Lilly, W.W. and Pukkila, P.J.
TITLE Expressed sequence tags from Coprinus cinereus (Coprinopsis
cinerea) cDNAs, spring 2005
JOURNAL Unpublished (2005)
COMMENT Contact: Gathman AC
Biology Department
Southeast Missouri State University
1 University Plaza, Cape Girardeau, MO 63701, USA
Tel: 5736512361
Fax: 573 651 2382
Email: agathman@semo.edu.

FEATURES
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XhoI; Mycelia grown for three days at 37 degrees on
minimal medium, then transferred to pre-warmed minimal
media and incubated at 42 degrees for one hour before
harvesting."

ORIGIN

Query Match 3.8%; Score 21; DB 8; Length 582;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 GAGCAACGATTAAAGCCCGT 66
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Db 469 GAGCAACGATTAAAGCCCGT 449

```

RESULT 6
AQ37789/c
LOCUS      AQ37789
DEFINITION RPEC11-6406.TK RPEC1-11 Homo sapiens genomic clone RPEC1-11-6406,
            genomic survey sequence.
ACCESSION  AQ37789
VERSION    AQ37789.1
KEYWORDS   GI:3670080
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 609)
            Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
            Use of human BAC End Sequences for Sequence-Ready Map Building
            Unpublished (1998)
JOURNAL    Other GSSs: RPEC11-6406.TU
COMMENT    Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are derived from the human BAC library RPEC1-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.

FEATURES
            source
            1..609
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="GDB:7524533"
            /db_xref="taxon:9606"
            /clone="RPEC1-11-6406"
            /sex="Male"
            /cell_type="Lymphocytes"
            /clone_lib="RPEC1-11"
            /note="Vector: pBAC3 6; Site_1: EcoRI; Site_2: EcoRI;
            RPEC11 Human Male BAC Library"

ORIGIN
Query Match      3.8%; Score 21; DB 9; Length 609;
Best Local Similarity 100.0%; Pred.No.18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        224 AATATATCTTCCAAATATAAA 204

RESULT 7
CE361611/c
LOCUS      CE361611
DEFINITION tigr-gss-dog-17000361532982 Dog library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION  CE361611
VERSION    CE361611.1
KEYWORDS   GI:36575419
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
            1 (bases 1 to 637)
            Kirtness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,

FEATURES
            source
            1..637
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /strain="Standard Poodle"
            /db_xref="taxon:9615"
            /clone_lib="Dog Library"
            /note="Site 1: BstXI; Libraries were prepared from
            peripheral blood"

ORIGIN
Query Match      3.8%; Score 21; DB 10; Length 637;
Best Local Similarity 100.0%; Pred.No.18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        342 AATATATCTTCCAAATATAAA 322

RESULT 8
CR825238/c
LOCUS      CR825238
DEFINITION GR09AA56BC03FW2 INRA BAC Bos taurus genomic clone INRA8_1005H12,
            DNA sequence, genomic survey sequence.
ACCESSION  CR825238
VERSION    CR825238.1
KEYWORDS   GI:52761326
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
            1 (bases 1 to 779)
            Eggen,A., Schibler,L. and Roy,A.
            Bovine BAC End Sequences from the INRA bovine BAC library
            Unpublished
            2 (bases 1 to 779)
            Genoscope.
            Direct Submission
            Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
            Contact: Andre Eggen
            Department of Animal Genetics - LGDC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 1005 row: H column: 12
            Seq primer: M13 Forward
            Class: BAC ends.

FEATURES
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            /mol_type="genomic DNA"
            /strain="Standard Poodle"
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            /clone_lib="Dog Library"
            /note="Site 1: BstXI; Libraries were prepared from
            peripheral blood"

ORIGIN
Query Match      3.8%; Score 21; DB 10; Length 637;
Best Local Similarity 100.0%; Pred.No.18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        342 AATATATCTTCCAAATATAAA 322

```

```

TITLE      Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
JOURNAL    Venter,J.C.
PUBMED     The dog genome: survey sequencing and comparative analysis
            Science 301 (5641), 1898-1903 (2003)
14512627
COMMENT    Contact: Kirtness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirtness@tigr.org
            Class: shotgun.

FEATURES
            source
            1..637
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /strain="Standard Poodle"
            /db_xref="taxon:9615"
            /clone_lib="Dog Library"
            /note="Site 1: BstXI; Libraries were prepared from
            peripheral blood"

ORIGIN
Query Match      3.8%; Score 21; DB 10; Length 637;
Best Local Similarity 100.0%; Pred.No.18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        342 AATATATCTTCCAAATATAAA 322

RESULT 8
CR825238/c
LOCUS      CR825238
DEFINITION GR09AA56BC03FW2 INRA BAC Bos taurus genomic clone INRA8_1005H12,
            DNA sequence, genomic survey sequence.
ACCESSION  CR825238
VERSION    CR825238.1
KEYWORDS   GI:52761326
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
            1 (bases 1 to 779)
            Eggen,A., Schibler,L. and Roy,A.
            Bovine BAC End Sequences from the INRA bovine BAC library
            Unpublished
            2 (bases 1 to 779)
            Genoscope.
            Direct Submission
            Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
            Contact: Andre Eggen
            Department of Animal Genetics - LGDC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 1005 row: H column: 12
            Seq primer: M13 Forward
            Class: BAC ends.

FEATURES
            source
            1..779
            /organism="Bos taurus"
            /mol_type="genomic DNA"
            /strain="Standard Poodle"
            /db_xref="taxon:9615"
            /clone_lib="Dog Library"
            /note="Site 1: BstXI; Libraries were prepared from
            peripheral blood"

ORIGIN
Query Match      3.8%; Score 21; DB 10; Length 637;
Best Local Similarity 100.0%; Pred.No.18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        342 AATATATCTTCCAAATATAAA 322

```

/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Holstein"
/db_xref="taxon:9913"
/clone="INRAD_1005H12"
/sex="Male"
/cell_type="fibroblast"
/clone_1ib="INRA bovine BAC"
/note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
INRA Bovine BAC library (Male) produced by Andre Eggen
Genoscope sequence ID : GR05AA56BC03FM2"

ORIGIN

Query Match 3.8%; Score 21; DB 11; Length 779;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TTGAAGATCATATGATGTT 249
|||||
Db 306 TTGAAGATCATATGATGTT 286

RESULT 9
DN590945/c
LOCUS 92028.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
DEFINITION 92028.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
ACCESSION DN590945
VERSION DN590945
KEYWORDS EST
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum (potato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanales; Solanales; Solanum.
1 (bases 1 to 902)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De
Koeyer, D., Andy, P., Goyer, C., Li, X.-Q., Wang, Pruski, G. and Regan, S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
CONTACT: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
Location/Qualifiers
1..902
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="92028"
/issue_type="Tubers"
/lab_host="X110-Gold"
/clone_1ib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+); XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996). Genome Research 6: 791-806."

FEATURES

source

ORIGIN

Query Match 3.8%; Score 21; DB 8; Length 902;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 AGAAGAGAGAAATACAAAGT 380
|||||
Db 587 AGAAGAGAGAAATACAAAGT 567

RESULT 10
BF475913/c
LOCUS 208 bp mRNA
DEFINITION naa14e07.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3254869 3'
similar to TR_015355 Q15355 SKELETAL MUSCLE ABUNDANT PROTEIN. ;,
mRNA sequence.
BF475913
VERSION BF475913.1 GI:11546740
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 208)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA library preparation: M. Bento Soares, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..208
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3254869"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="NCI-CCAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and as
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.6%; Score 20; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 AGCGGTACAGAGGCTCTTG 487
|||||
Db 164 AGCGGTACAGAGGCTCTTG 145

RESULT 11

AG191545/c
LOCUS 220 bp DNA
DEFINITION Pan troglodytes DNA, clone: RP43-067122.T7, genomic survey
sequence.


```

ACCESSION   AG191545
VERSION     AG191545.1  GI:45223721
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pan.
REFERENCE   1
AUTHORS     Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE       BAC end sequences of library RP-43
JOURNAL     Unpublished
AUTHORS     2 (bases 1 to 220)
            Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE       Direct Submision
JOURNAL     Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
            52, Qun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
            Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the Red process and may have higher chance
            of clone tracking errors.
COMMENT     PRIMERS
            Sequencing: T7
LIBRARY     Vector : pBac3.6
            R.Site 1 : EcoRI
            R.Site 2 : EcoRI.
FEATURES     source
            1..220
            Location/Qualifiers
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="RP43-067122.T7"
                /sex="male"
                /cell_type="lymphocytes"
                /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match      3.6%; Score 20; DB 10; Length 220;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      392 ATTAATCTAGAAATTCAGAA 411
Db      |||||||||||||||||||
        33 ATTAATCTAGAAATTCAGAA 14

RESULT 12
LOCUS      CX630648/c 326 bp mRNA linear EST 14-JAN-2005
DEFINITION GNM001F05r GNW Hordeum vulgare cDNA clone GNM001F05 5-PRIME, mRNA
SEQUENCE.
ACCESSION  CX630648
VERSION    CX630648.1 GI:57829435
KEYWORDS  EST.
SOURCE     Hordeum vulgare
ORGANISM  Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 326)
Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,
Schaefer, W., Scholz, U., Sonnwald, U. and Kogel, K.H.
Barley ESTs from different tissues challenged with fungal pathogens
Unpublished (2004)
Contact: Sophia Biemelt
Molecular Developmental Physiology, Department Molecular Cell
Biology
Institute of Plant Genetics and Crop Plant Research (IPK)

FEATURES     source
            1..352
            Location/Qualifiers
                /organism="Hordeum vulgare"

```

```

Corrensstr. 3, 06466 Gatersleben, Germany
Tel: +49 (0)39482-5476
Fax: +49 (0)39482-5515
Email: biemelt@ipk-gatersleben.de
Insert Length: 326 Std Error: 0.00
Plate: 1 row: F column: 5
Seq primer: M3rev.
FEATURES     source
            1..326
            Location/Qualifiers
                /organism="Hordeum vulgare"
                /mol_type="mRNA"
                /cultivar="Nickel"
                /db_xref="GABI:958984"
                /db_xref="taxon:4513"
                /clone="GNM001F05"
                /tissue_type="roots"
                /lab_host="E. coli BM25.8"
                /clone_lib="GNW"
                /note="Vector: pTRIPLEX2; Site 1: Sfi IA; Site 2: Sfi IB;
                roots, seedlings were grown in a mixture of SERAMIS and
                OIL DRI soil at 20 degr. C, 16h light and 50-60% rel.
                humidity for 7 days, Roots were harvested 6, 24, 48, 72,
                and 96 hpi (hours post inoculation) with Fusarium culmorum
                KF 350. PolyA-RNA was isolated from water treated roots
                and used to create a cDNA-library by means of the SMART
                cDNA library construction kit (CLONTECH). cDNA fragments
                were inserted into the vector lambda Triplex Sfi I.
                Subsequently, plasmids were obtained by in vivo excision
                according to manufacturers instruction. (GABI-Agrotech
                Project)"

ORIGIN
Query Match      3.6%; Score 20; DB 8; Length 326;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      137 TTATTGTGAATGATGCA 156
Db      |||||||||||||||||||
        95 TTATTGTGAATGATGCA 76

RESULT 13
LOCUS      CX630668 352 bp mRNA linear EST 14-JAN-2005
DEFINITION GNM001G04r GNW Hordeum vulgare cDNA clone GNM001G04 5-PRIME, mRNA
SEQUENCE.
ACCESSION  CX630668
VERSION    CX630668.1 GI:57829455
KEYWORDS  EST.
SOURCE     Hordeum vulgare
ORGANISM  Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 352)
Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,
Schaefer, W., Scholz, U., Sonnwald, U. and Kogel, K.H.
Barley ESTs from different tissues challenged with fungal pathogens
Unpublished (2004)
Contact: Sophia Biemelt
Molecular Developmental Physiology, Department Molecular Cell
Biology
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466 Gatersleben, Germany
Tel: +49 (0)39482-5476
Fax: +49 (0)39482-5515
Email: biemelt@ipk-gatersleben.de
Insert Length: 352 Std Error: 0.00
Plate: 1 row: G column: 4
Seq primer: M3rev.
FEATURES     source
            1..352
            Location/Qualifiers
                /organism="Hordeum vulgare"

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/mol_type="mRNA"
/cultivar="Nickel"
/db_xref="GABI:959004"
/db_xref="taxon:4513"
/clone="GNM001G04"
/issue_type="roots"
/lab_host="E. coli BM25.8"
/clone_1ib="GNM"
/note="Vector: pTriplex2; Site_1: Sfi IA; Site_2: Sfi IB;
roots. Seedlings were grown in a mixture of SERAMIS and
Oli DRI soil at 20 degr. C, 16h light and 50-60% rel.
humidity for 7 days. Roots were harvested 6, 24, 48, 72,
and 96 hpi (hours post inoculation) with Fusarium culmorum
KF 350. PolyA-RNA was isolated from water treated roots
and used to create a cDNA-library by means of the SMART
cDNA library construction kit (CLONTECH). cDNA fragments
were inserted into the vector Lambda Triplex Sfi I.
Subsequently, plasmids were obtained by in vivo excision
according to manufacturers instruction. (GABI-Agrotech
Project)"

ORIGIN

Query Match      3.6%; Score 20; DB 8; Length 352;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      137 TTTATTGTGATGATGCGCA 156
      |||||
      85 TTTATTGTGATGATGCGCA 66

RESULT 14
LOCUS      A0832728      398 bp      DNA      linear      GSS 27-AUG-1999
DEFINITION HS_3238_A1_B11_MR_CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3238 Col=21 Row=C, genomic survey
sequence.
ACCESSION  A0832728
VERSION    A0832728.1  GI:5798790
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 398)
            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
            Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
            Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
            10449764
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htec.washington.edu
            Plate: 3238 row: C column: 21
            Seg primer: M13 Reverse
            Class: BAC ends
            High quality sequence stop: 398.
            Location/Qualifiers
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                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="Plate=3238 Col=21 Row=C"
                        /sex="male"
```

```
/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match      3.6%; Score 20; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      225 TGTTTTGAAGATCATATCG 244
      |||||
      234 TGTTTTGAAGATCATATCG 215

RESULT 15
LOCUS      BF843865      471 bp      mRNA      linear      EST 13-JAN-2001
DEFINITION MR1-HT1184-181200-001-f12 HT1184 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF843865
VERSION    BF843865.1  GI:12198863
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 471)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            10737800
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&c2=MR1-HT1184-
            181200-001-f12&t3=2000-12-18&t4=1)
            Seg primer: puc 18 forward
            High quality sequence stop: 8
            High quality sequence stop: 471.
            Location/Qualifiers
                source
                    1..471
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /dev_stage="Adult"
                        /clone_1ib="HT1184"
                        /note="Organ: head_neck; Vector: puc18; Site_1: Sma1;
                        Site_2: Sma1; A mini-library was made by cloning products
                        derived from ORSSTES PCR (U.S. Letters Patent application
                        No. 196,716 - Ludwig Institute for Cancer Research)
                        profiles into the pUC 18 vector. Reverse transcription of
                        tissue mRNA and cDNA amplification were performed under
                        low stringency conditions."
```

```
ORIGIN

Query Match      3.6%; Score 20; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      270 AGTACTGAAGCTTCACATG 289
```

Db 282 AGTAGCTGAAGCTTCACCTG 301

RESULT 16
LOCUS CN846247/c 480 bp mRNA linear EST 02-JUN-2004
DEFINITION PG07010F11 Ginseng cDNA library from MeJa treated hairy root Panax
ACCESSION CN846247
VERSION CN846247
KEYWORDS EST. 47963538
SOURCE Panax ginseng
ORGANISM Panax ginseng
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Apiales; Araliaceae; Panax.
1 (bases 1 to 480)
Choi,D.W., Jung,J.D., Ha,Y.I., Park,H.W., In,D.S., Chung,H.J. and
Jiu,J.R.
TITLE Analysis of transcripts in methyl jasmonate-treated ginseng hairy
roots to identify genes involved in the biosynthesis of
ginsenosides and other secondary metabolites
JOURNAL Unpublished (2004)
COMMENT Contact: Dong-Woog Choi
Eugentech / KRIBB
52 Oun-dong, Yusong-Gu, Daejeon 305-333, Korea
Tel: 82 42 863 2051
Fax: 82 42 863 2049
Email: dwchoi@eugentech.com
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
High quality sequence stop: 480
POLY-A-No.

FEATURES
source Location/Qualifiers
1..480
/organism="Panax ginseng"
/mol_type="mRNA"
/db_xref="taxon:4054"
/clone="PG07010F11"
/cissue_type="MeJa treated hairy root"
/clone_lib="Ginseng cDNA library from MeJa treated hairy
root"
/note="Vector: lambda ZAP XR; cDNAs from MeJa treated
ginseng hairy root were cloned into lambda ZAP XR vector"

ORIGIN
Query Match 3.6%; Score 20; DB 7; Length 480;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 TCAATTATCTTCCAAATA 190
|||||
145 TCAATTATCTTCCAAATA 126
|||||

Db 171 TCAATTATCTTCCAAATA 190
|||||
145 TCAATTATCTTCCAAATA 126
|||||

RESULT 17
LOCUS BB665726 546 bp mRNA linear EST 25-APR-2001
DEFINITION BB665726
ACCESSION BB665726
VERSION BB665726.1 GI:10026317
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 546)
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Caase,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,

Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPJ
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 68 row: G column: 22
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1..546
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NctI, Site 2: SalI;
library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN
Query Match 3.6%; Score 20; DB 2; Length 546;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 AGCAGAGGCTCTGGGATTG 493
|||||
480 AGCAGAGGCTCTGGGATTG 499
|||||

Db 474 AGCAGAGGCTCTGGGATTG 493
|||||
480 AGCAGAGGCTCTGGGATTG 499
|||||

RESULT 18
LOCUS BM289207 556 bp mRNA linear EST 28-DEC-2001
DEFINITION BM289207
ACCESSION BM289207
VERSION BM289207.1 GI:17998233
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 556)
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Caase,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPJ
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCAGCAGC
 Plate: 144 row: 1 column: 4
 Seq primer: ATTAGTGTCACTATATG.
 Location/Qualifiers

FEATURES

source

1..556
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /cissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 380V"
 /note="Vector: pCMV SPORTe; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."

ORIGIN

Query Match 3.6%; Score 20; DB 3; Length 556;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 AGCAGAGGCTCTGGATTG 493
 |||||
 Db 429 AGCAGAGGCTCTGGATTG 448

RESULT 19

AO702954/c

LOCUS AO702954 558 bp DNA linear GSS 07-JUL-1999
 DEFINITION HS_5443_B1_B12_T7A RPCI-11 Human Male BAC Library Homo sapiens
 genomic clone Plate=1019 Col=23 Row=D, genomic survey sequence.
 ACCESSION AO702954
 VERSION AO702954.1 GI:5412380
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 558)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3867
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end web Server:
 http://www.htsc.washington.edu
 Plate: 1019 row: D column: 23
 Seq primer: T7
 Class: BAC end
 High quality sequence stop: 558.
 Location/Qualifiers

FEATURES

source

1..558
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=1019 Col=23 Row=D"

JOURNAL

PUBMED

COMMENT

COMMENT

TITLE

TITLE

FEATURES

source

1..558
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=1019 Col=23 Row=D"

/sex="male"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 3.6%; Score 20; DB 9; Length 558;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 211 GGAGTGATTGTAAATGTTT 230
 |||||
 Db 41 GGAGTGATTGTAAATGTTT 22

RESULT 20

BM220108

LOCUS BM220108 587 bp mRNA linear EST 02-JUN-2005
 DEFINITION BM220108 Nori Satoh unpublished cDNA library, egg Ciona
 intestinalis cDNA clone c1eg098g07 5', mRNA sequence.
 ACCESSION BM220108
 VERSION BM220108.1 GI:24736531
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cloniidae; Ciona.
 1 (bases 1 to 587)
 Satou,Y., Shin,I.T., Kohara,Y. and Satoh,N.
 Expressed genes in Ciona intestinalis (2002c)
 Unpublished (2002)
 Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@scidian.zool.kyoto-u.ac.jp.
 Location/Qualifiers

FEATURES

source

1..587
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="c1eg098g07"
 /cissue_type="whole animal"
 /dev_stage="egg"
 /clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN

Query Match 3.6%; Score 20; DB 5; Length 587;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AAAGAGGCTGTGATTAGA 125
 |||||
 Db 484 AAAGAGGCTGTGATTAGA 503

RESULT 21

BM355953

LOCUS BM355953 594 bp mRNA linear EST 27-MAY-2004
 DEFINITION BM355953 Yutaka Satou unpublished cDNA library, mature adult whole
 animal Ciona intestinalis cDNA clone c1ma808g18 5', mRNA sequence.
 ACCESSION BM355953
 VERSION BM355953.1 GI:47767754
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cloniidae; Ciona.

REFERENCE 1 (bases 1 to 594)
 AUTHORS Satou,Y., Shin-I.,T., Kohara,Y. and Satoh,N.
 TITLE Expressed genes in *Ciona intestinalis* (2004)
 JOURNAL Unpublished (2004)
 COMMENT Contact: Yutaka Satou
 Department of Zoology
 Kyoto University
 Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4095
 Fax: 81-75-705-1113
 Email: yutaka@sci.kyoto-u.ac.jp.

FEATURES
 source
 1..594
 Location/Qualifiers

/organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="cima808918"
 /tissue_type="whole animal"
 /dev_stage="mature adult"
 /clone_lib="Yutaka Satou unpublished cDNA library, mature adult whole animal"

ORIGIN

Query Match 3.6%; Score 20; DB 5; Length 594;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 AAAGAGCTGCTGATTGA 125
 |||||
 Db 260 AAAGAGCTGCTGATTGA 279

RESULT 22
 DT014963/c 599 bp mRNA linear EST 05-AUG-2005

LOCUS DT014963 599 bp mRNA linear EST 05-AUG-2005
 DEFINITION VV1094GG4.597394 Cabsau Flower Stage 12 (FL0u0012) vitis vinifera
 CDNA clone VV1094G04 5, mRNA sequence.

ACCESSION DT014963
 VERSION DT014963.1 GI:71865908
 KEYWORDS EST.

SOURCE
 ORGANISM

Vitis vinifera
 Vitis vinifera
 Bukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 599)

REFERENCE Iocco,P., Hua,C., Davies,C. and Thomas,M.R.
 AUTHORS
 TITLE Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon

JOURNAL Unpublished (2003)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR Primers
 FORWARD: T7 20mer (forward)
 BACKWARD: SP6 18mer
 Plate: 094 row: G column: 04
 Seq primer: T7 20mer (forward)
 High quality sequence stop: 599.

FEATURES

source

1..599
 Location/Qualifiers
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="VV1094G04"
 /sex="Hermaphrodite"
 /dev_stage="12 - modified E-L system"
 /clone_lib="Cabsau Flower Stage 12 (FL0u0012)"

ORIGIN

Query Match 3.6%; Score 20; DB 8; Length 599;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 AAGAGTTGCAGAGAGAGA 369
 |||||
 Db 116 AAGAGTTGCAGAGAGAGA 97

RESULT 23

CL347309 650 bp DNA linear GSS 19-AUG-2004
 LOCUS RPCI44_272M24.f RPCI-44 Sus scrofa genomic clone RPCI44_272M24,
 DEFINITION genomic survey sequence.

ACCESSION CL347309

VERSION CL347309.1 GI:51399278

KEYWORDS GSS.

SOURCE Sus scrofa (pig)

ORGANISM

Bukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE 1 (bases 1 to 650)
 AUTHORS Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
 Beaver,J.E. and Schock,L.B.
 TITLE Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
 JOURNAL Through Comparative Genomics
 COMMENT Unpublished (2004)
 Other GSSs: RPCI44_272M24.f
 Contact: Lawrence B. Schock
 Department of Animal Sciences
 University of Illinois at Urbana Champaign
 1201 W. Gregory Dr., Urbana, IL 61801, USA
 Tel: 217 265 5326
 Fax: 217 244 5617
 Email: schock@uiuc.edu

Classes are derived from the porcine BAC library RPCI-44
 (http://www.bacpac.chori.org/porcine242.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@chori.org).
 Clones may be purchased from BACPAC Resources
 (http://BACPACresources.chori.org). This work was undertaken as part
 of the International Swine Genome Sequencing Consortium by
 University of Illinois at Urbana Champaign, USA with funds provided
 by grant No. AG2002-34480-11828 from USDA-CRSRS and
 AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
 Initiative)
 Plate: 272 row: M column: 24
 Seq primer: 17

Classes: BAC ends.

Location/Qualifiers

FEATURES

source

1..650
 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="genomic DNA"
 /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
 Weibnan)"
 /db_xref="taxon:9823"
 /clone="RPCI44_272M24"
 /sex="male"
 /cell_type="blood"
 /clone_lib="RPCI-44"
 /note="Vector: pTARBAC2, Site_1: EcoRI, Site_2: EcoRI;
 porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match 3.6%; Score 20; DB 10; Length 650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 ATCTTCCAAATTAATGAT 197
|||||
Db 272 ATCTTCCAAATTAATGAT 291
|||||

RESULT 24
DT014681/c 652 bp mRNA linear EST 05-AUG-2005
LOCUS VVI091D02.596830 Cabsau Flower Stage 12 (FLOU0012) Vitis vinifera
DEFINITION CDNA clone VVI091D02 5, mRNA sequence.
ACCESSION DT014681
VERSION DT014681.1 GI:71865626
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 652)
Iocco, P., Hua, C., Davies, C. and Thomas, M.R.
Expressed sequence tags from the grapevine cultivar Cabernet
Sauvignon
Unpublished (2003)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7 20mer (forward)
BACKWARD: SP6 18mer
Place: 091 row: D column: 02
Seq primer: T7 20mer (forward)
High quality sequence stop: 652.
Location/Qualifiers
1..652
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="VVI091D02"
/sex="Hermaphrodite"
/dev_stage="12 - modified E-L system"
/clone_lib="Cabsau Flower Stage 12 (FLOU0012)"
/note="Organ: Inflorescence including flowers; Vector:
pZL; A cDNA library from immature inflorescences at stage
12 of the modified E-L system. Tissue collected from
field grown plants. A description of the modified E-L
system can be found in the paper by B. G. Coombe
'Adoption of a system for identifying grapevine growth
stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN

Query Match 3.6%; Score 20; DB 8; Length 652;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 AAGAGTTGCAGAGAGAGA 369
|||||
Db 133 AAGAGTTGCAGAGAGAGA 114
|||||

RESULT 25
AF062715 721 bp mRNA linear EST 03-MAY-1999
LOCUS AF062715 Homo sapiens library (Yu Y) Homo sapiens cDNA clone
DEFINITION HA0033, mRNA sequence.

ACCESSION AF062715
VERSION AF062715.1 GI:4731771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 721)
Yu, Y., Dong, C. and He, F.
Finding some ESTs
Unpublished (1998)
Contact: Yongtao Yu
Department of Hematology
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
Fax: 0086-10-68214653
Email: yu48@yahoo.com.
Location/Qualifiers
1..721
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HA0033"
/clone_lib="Homo sapiens library (Yu Y)"

ORIGIN

Query Match 3.6%; Score 20; DB 1; Length 721;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCAGTGTGTTGAATG 226
|||||
Db 141 TGTTCAGTGTGTTGAATG 122
|||||

RESULT 26
A1110607 721 bp mRNA linear EST 11-NOV-1999
LOCUS HA0033 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
DEFINITION A1110607
ACCESSION A1110607.1 GI:6359472
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 721)
Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
and He, F.
Expression profile analysis of a human fetal liver cDNA library
Unpublished (1999)
Contact: Yongtao Yu
Department of Hematology
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
Fax: 0086-10-68214653
Email: yu48@yahoo.com.
Location/Qualifiers
1..721
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="fetal"
/dev_stage="fetal"
/lab_host="MC1061/P3"
/clone_lib="Human fetal liver cDNA library"
/note="Vector: pCDNA1"

ORIGIN

```

Query Match      3.6%; Score 20; DB 1; Length 721;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 TGTGGAGTGATTGTAATG 226
    |||||
    141 TGTGGAGTGATTGTAATG 122

RESULT 27
AGS94544      774 bp      DNA      linear      GSS 23-DEC-2004
LOCUS      Mus musculus molossinus DNA, clone:MSWg01-524H14.TJ, genomic survey
DEFINITION      sequence.
ACCESSION      AGS94544
VERSION      AGS94544.1 GI:48355374
KEYWORDS      GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
ORGANISM      Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
            Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
            Genome Res. 14 (12), 2439-2447 (2004)

JOURNAL
PUBMED      15574823
REFERENCE      2 (bases 1 to 774)
AUTHORS      Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE      Direct Submission
            Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suenhiro-chou,Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Clones are derived from the mouse BAC library MSWg01. For BAC
            library availability, please contact Kunjia Abe (abe@tc.riken.jp).
            Tsukuba Institute, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koydai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY      : PBACe3.6
Vector       : EcoRI
R.Site 1    : EcoRI
R.Site 2    : EcoRI.
FEATURES
    source
        1..774
            /organism="Mus musculus molossinus"
            /mol_type="genomic DNA"
            /sub_species="molossinus"
            /db_xref="taxon:57486"
            /clone="MSWg01-524H14.TJ"
            /sex="male"
            /issue_type="mixture of kidney and spleen"
            /clone_lib="MSWg01 Mouse Male BAC Library"

ORIGIN
Query Match      3.6%; Score 20; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 GGTAGAGAGGCTCTTGGA 490
    |||||
    82 GGTAGAGAGGCTCTTGGA 101

```

```

RESULT 28
BZ717132/C      797 bp      DNA      linear      GSS 24-FEB-2003
LOCUS      PUCGG02TD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa139B03,
DEFINITION      genomic survey sequence.
ACCESSION      BZ717132
VERSION      BZ717132.1 GI:28502185
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 797)
REFERENCE
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
            Benick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennezen,J.
            Maize Genomics Consortium
            Unpublished (2003)
TITLE      Contact: Cathy Whitelaw
JOURNAL
COMMENT      TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@cigr.org
            Seq primer: TP
            Class: sheared ends.
FEATURES
    source
        1..797
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBTa139B03"
            /clone_lib="ZM_0.6_1.0_KB"
            /note="Vector: PCR4-TOPO, Site 1: EcoRI; 0.6-1.0 kb high
            COT selected genomic DNA library"

ORIGIN
Query Match      3.6%; Score 20; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 ATTATCTCCAAATTAAT 194
    |||||
    577 ATTATCTCCAAATTAAT 558

RESULT 29
CC855478      815 bp      DNA      linear      GSS 24-JUL-2003
LOCUS      ND.L.36C7.SP6 Notre Dame Liverpool Aedes aegypti genomic clone
DEFINITION      NotreDame Liverpool-36C7, genomic survey sequence.
ACCESSION      CC855478
VERSION      CC855478.1 GI:33211395
KEYWORDS      GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM      Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
            Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
            1 (bases 1 to 815)
REFERENCE
AUTHORS      Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE      BAC end sequencing of Aedes aegypti
JOURNAL      Unpublished (2003)
COMMENT      Other GSSes: ND.L.36C7.T7
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208

```


Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.

FEATURES

source
Location/Qualifiers

1..815
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="Notredame Liverpool-36C7"
/clone_1lb="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site.1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match 3.6%; Score 20; DB 9; Length 815;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 CTGATTAGACGACGACGA 135
|||||
Db 557 CTGATTAGACGACGACGA 576

RESULT 30 974 bp mRNA linear EST 02-APR-2003
CB558744/c
LOCUS
DEFINITION
IMAGE:4030758 5', mRNA sequence.
ACCESSION
CB558744
VERSION
CB558744.1 GI:29478274
KEYWORDS
EST.

SOURCE
ORGANISM
Xenopus laevis (African clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 974)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLAM9297 row: b column: 07
High quality sequence stop: 376.

FEATURES

source

Location/Qualifiers
1..974
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGS:4030758"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NICHD XGC Kid1"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.2 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Query Match 3.6%; Score 20; DB 6; Length 974;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TAAATGTTTGAAGATCAT 240
|||||

Db 107 TAAATGTTTGAAGATCAT 88

RESULT 31

BH770411/c 1175 bp DNA linear GSS 01-MAY-2002
LMGtag184 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.

DEFINITION

ACCENSION
BH770411
VERSION
BH770411.1 GI:20373368
KEYWORDS
GSS.
Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.

REFERENCE
1 (bases 1 to 1175)
AUTHORS
TITLE
JOURNAL
COMMENT
Genetique Microbienne

INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is obgL (84%)
Class: Shotgun
High quality sequence start: 30
High quality sequence stop: 1147.

FEATURES

source

Location/Qualifiers
1..1175
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="cremoris"
/db_xref="taxon:1359"
/clone_1lb="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM02; Site.1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."

ORIGIN

Query Match 3.6%; Score 20; DB 9; Length 1175;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 GCTGCTGATTTGAAGCAGA 131
|||||
Db 408 GCTGCTGATTTGAAGCAGA 389

RESULT 32

CN351365 140 bp mRNA linear EST 16-MAY-2004
LOCUS
DEFINITION
17000532184997 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCENSION
CN351365
VERSION
CN351365.1 GI:47351299
KEYWORDS
EST.

SOURCE
ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 140)
Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fiek, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkoweki, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that

JOURNAL
PUBMED
15146197
COMMENT
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

CONTACT: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 140 Std Error: 0.00.
Location/Qualifiers

FEATURES
source
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_1ib="GRN_EB"
/note="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowth derived from h9 cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 3.4%; Score 19; DB 7; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGGAAATACAAAAGTGAT 383
|||||
47 AGGAAATACAAAAGTGAT 65

RESULT 33
BI033292/c 173 bp mRNA linear EST 14-JUN-2001
LOCUS PM2-NN0088-110201-003-f12 NN0088 Homo sapiens cDNA, mRNA sequence.
DEFINITION BI033292
ACCESSION BI033292.1 GI:114439918
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 173)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&ct=PM2-NN0088-
110201-003-f12&ct=2001-02-11&ct=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 173.
Location/Qualifiers

FEATURES

source

1. .173
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="NN0088"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESSES PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGGAAATACAAAAGTGAT 383
|||||
154 AGGAAATACAAAAGTGAT 136

RESULT 34
BI315574/c 231 bp mRNA linear EST 21-JUL-2004
LOCUS sa774b08.y1 Gm-cl078 Glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION ID: Gm-cl078-1983 5', mRNA sequence.
ACCESSION BI315574
VERSION BI315574.1 GI:14989893
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 231)

REFERENCE
AUTHORS Shoemaker, R., Kern, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE Public Soybean EST Project
JOURNAL Contact: Shoemaker R/Public Soybean EST Project
COMMENT Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Putative full
length read vector to vector length is 243 This clone is available
through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA
(phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco.
Location/Qualifiers

FEATURES
source

1. .231
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Brags NTS382"
/db_xref="taxon:3847"
/cissue_type="Roots of 7 day old 'Brags' supermodulating
mutant NTS382 seedlings"
/dev_stage="7 days old"
/lab_host="PH10B"
/clone_1ib="Gm-cl078"
/note="Vector: pBluescript II SK+, Site 1: EcoRI; Site 2:

XhoI; The mRNA was isolated from roots of 7 day old 'Bragg' supermodulating mutant NT8382 seedlings that were infected with Bradyrhizobium japonicum, strain USA 110, 48 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAGACTGCTGAG(7)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."

ORIGIN

Query Match 3.4%; Score 19; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 CATATATGACCTTACT 317
|||||
Db 136 CATATATGACCTTACT 118

RESULT 35
BX501946 239 bp mRNA linear EST 04-SEP-2003
DEFINITION DKF2p779P1265_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION BX501946
VERSION BX501946.1 GI:32022762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 239)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Oesanger,A., Fobo,G., Han,M., and Wiemann,S.
EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
COMMENT Contact: MIPS

FEATURES
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No SI sequence available.
This clone (DKF2p779P1265) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

source

1. 239
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p779P1265"
/issue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Query Match 3.4%; Score 19; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGAGAAATACAAAGTGAT 383
|||||
Db 147 AGAGAAATACAAAGTGAT 165

RESULT 36
BE695762 354 bp mRNA linear EST 11-SEP-2000
LOCUS QV0-CT0225-280700-307-e06 CT0225 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE695762
ACCESSION BE695762
VERSION BE695762.1 GI:10082974
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
Dias Neto,B., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coiera,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongseneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and Simpson,A.J.

REFERENCE

AUTHORS Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=ct2=QV0-CT0225-280700-307-e06&t3=2000-07-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 68
High quality sequence start: 202.
Location/Qualifiers

JOURNAL

PUBMED

COMMENT

FEATURES

source

1. 354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="CT0225"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from OESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 354;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 AATGCTCATCCGATCCAG 541
 |||||
 DB 32 AATGCTCATCCGATCCAG 50

RESULT 37

COL174612 357 bp mRNA linear EST 18-JUN-2004
 LOCUS ND1L_45 D06_b1 A029 Needles control Pinus taeda cDNA clone
 DEFINITION ND1L_45 D06_A029 3', mRNA sequence.

ACCESSION COL174612
 VERSION COL174612.1 GI:48947484
 KEYWORDS EST.
 SOURCE Pinus taeda (loblolly pine)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Pinus taeda
 Spermaphyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 1 (bases 1 to 357)
 Pratt, L., Cordomier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and
 Dean, J.F.D.
 An EST database from untreated loblolly pine (Pinus taeda) needles
 Unpublished (2004)
 Other ESTs: ND1L_45 D06_g1 A029
 Contact: Cordomier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpatt@uga.edu

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project a the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
 Seg primer: M13-21 (GTAAACGACGCGCACT)
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1..357
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="3 CCLONES"
 /db_xref="taxon:3352"
 /clone="ND1L_45 D06_A029"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Needles control"
 /note="Organ: needles; Vector: pSL1180; Site_1: EcorI; Site_2: XhoI; The library was prepared from polyA+ RNA from the needles of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Just before harvesting needles for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcorI (5' end) and XhoI (3' end)."

ORIGIN

Query Match

3.4%; Score 19; DB 7; Length 357;

Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 TCTTCCAAATTAATGAT 197
 |||||
 DB 310 TCTTCCAAATTAATGAT 328

RESULT 38

BI123660/c 386 bp mRNA linear EST 31-DEC-2001
 LOCUS 1026P75P Populus leaf cDNA library Populus tremula x Populus tremuloides cDNA, mRNA sequence.

ACCESSION BI123660
 VERSION BI123660.1 GI:18007635
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermaphyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 1 (bases 1 to 386)
 Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H.,
 Hillonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlert, R.,
 Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M.,
 Sandberg, G. and Lundberg, J.
 Gene expression in Populus
 Unpublished (2001)
 Contact: Erlandsson R
 Department of Biotechnology
 Royal Institute of Technology
 Teknikringen 30, Stockholm S-10044, Sweden
 Tel: 46 8 790 8287
 Fax: 46 8 245452
 Email: rikeri@biochem.kth.se.

TITLE
 JOURNAL
 COMMENT

Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /clone_lib="Populus leaf cDNA library"
 /note="Organ: leaf"

FEATURES

source

Location/Qualifiers
 1..386
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /clone_lib="Populus leaf cDNA library"
 /note="Organ: leaf"

ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 ATAAATGATTCACGCAA 206
 |||||
 DB 357 ATAAATGATTCACGCAA 339

RESULT 39

AL911633 399 bp mRNA linear EST 06-JUL-2004
 LOCUS AL911633 PUR-Z1+Z2 Danio rerio cDNA clone 034-C11-1, mRNA sequence.

ACCESSION AL911633
 VERSION AL911633.1 GI:23176903
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 399)
 Lo, J., Lee, S., Xu, M., Liu, F., Ruan, H., Eun, A., He, Y., Ma, W.,
 Wang, W., Wen, Z. and Peng, J.
 15000 unique zebrafish EST clusters and their future use in
 microarray for profiling gene expression patterns during
 embryogenesis
 Genome Res. 13 (3), 455-466 (2003)

TITLE

JOURNAL
 PUBMED

COMMENT

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Email: pengj@imcb.a-star.edu.sg
Clone requests: info@openbiosystems.com
Open Biosystems,
6705 Odyssey Drive, Huntsville, AL 35806.

FEATURES

Location/Qualifiers
1. 399

/organism="Danio rerio"
/mol_type="mRNA"
/strain="local wildtype"
/db_xref="taxon:7955"
/clone="034-C11-1"
/issue_type="whole embryo or fish"
/dev_stage="mixed stages"
/clone_1fb="PJR-Z1+Z2"

ORIGIN

Query Match 3.4%; Score 19; DB 1; Length 399;
Best Local Similarity 100.0%; Pred.No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 TGAATGTATGCAGTTCAA 162

Db 313 TGAATGTATGCAGTTCAA 295

RESULT 40

BM024201/c

LOCUS fu47d11.x1 zebrafish adult brain Danio rerio cDNA clone 399 bp mRNA linear EST 26-JUL-2002
IMAGE:5332653 3', mRNA sequence.

ACCESSION

BM024201

VERSION

BM024201.1 GI:16538557

KEYWORDS

EST.

SOURCE

Danio rerio (zebrafish)

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 399)

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)

TITLE

Contact: Stephen L. Johnson

JOURNAL

Washington University School of Medicine

COMMENT

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Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: John Ngai. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)

Seq primer: -40UP

High quality sequence stop: 346.

FEATURES

source

1. 399

Location/Qualifiers

/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5332653"

ORIGIN

Query Match 3.4%; Score 19; DB 3; Length 399;
Best Local Similarity 100.0%; Pred.No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 TGAATGTATGCAGTTCAA 162

Db 332 TGAATGTATGCAGTTCAA 314

/sex="mixed male and female"
/issue_type="brain"
/dev_stage="adult"
/lab_host="R. coli DH10B"
/clone_1fb="zebrafish adult brain"
/note="Vector: pZIRPlox; Site 1: NotI; Site 2: SalI;
excision of the cDNA library was performed in lambdaZIRPlox. Mass
pZIRPlox plasmids. Insert check was done in original
library."

Search completed: April 11, 2006, 21:45:45
Job time : 7767.45 secs

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